

5/1/42,628

WO 97/32980

1/90

42628

PCT/CA97/00163

APPROVED BY BRAFTSMAN	O.G. FIG.
	CLASS SU

AMINO ACID SEQUENCES OF A CONSERVED PORTION OF  
Tbp1 PROTEIN FOR CONSTRUCTION OF DEGENERATE  
PRIMERS USED IN PCR AMPLIFICATION OF A PORTION  
OF THE *M. cattarhalis* 4223 *tbpA* GENE.

N E V T G L G

SEQ ID NO: 17

G A I N E I E

SEQ ID NO: 18

FIG.1

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660750-2292760

APPROVED	O.G. FIG.	
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09/142628

*M. catarrhalis* 4223 Transferrin Receptor Genes

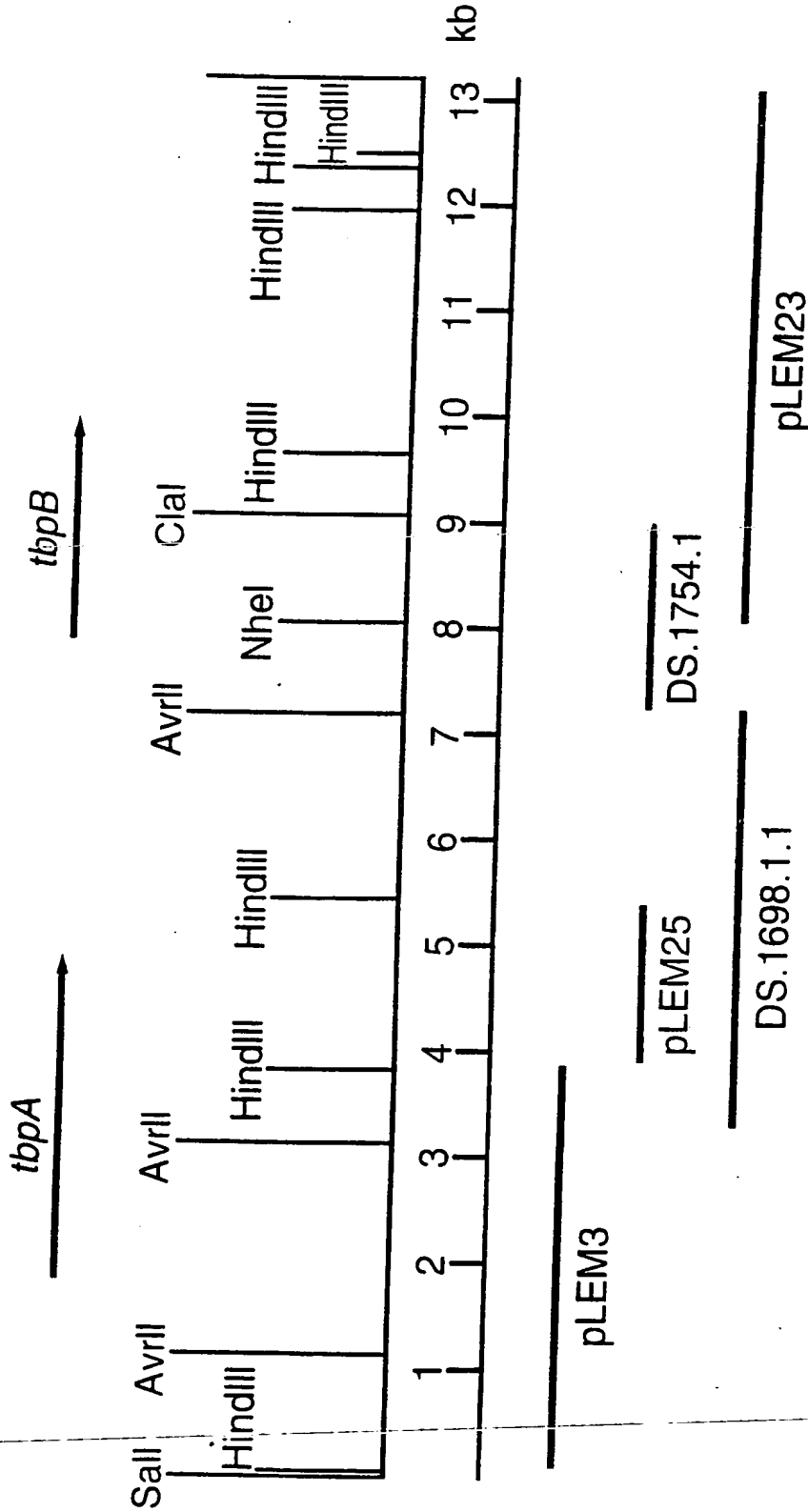


FIG.2

APPROVED	O.G. FIG.	
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60130-32980

*M. catarrhalis* 4223 *tbpA* gene

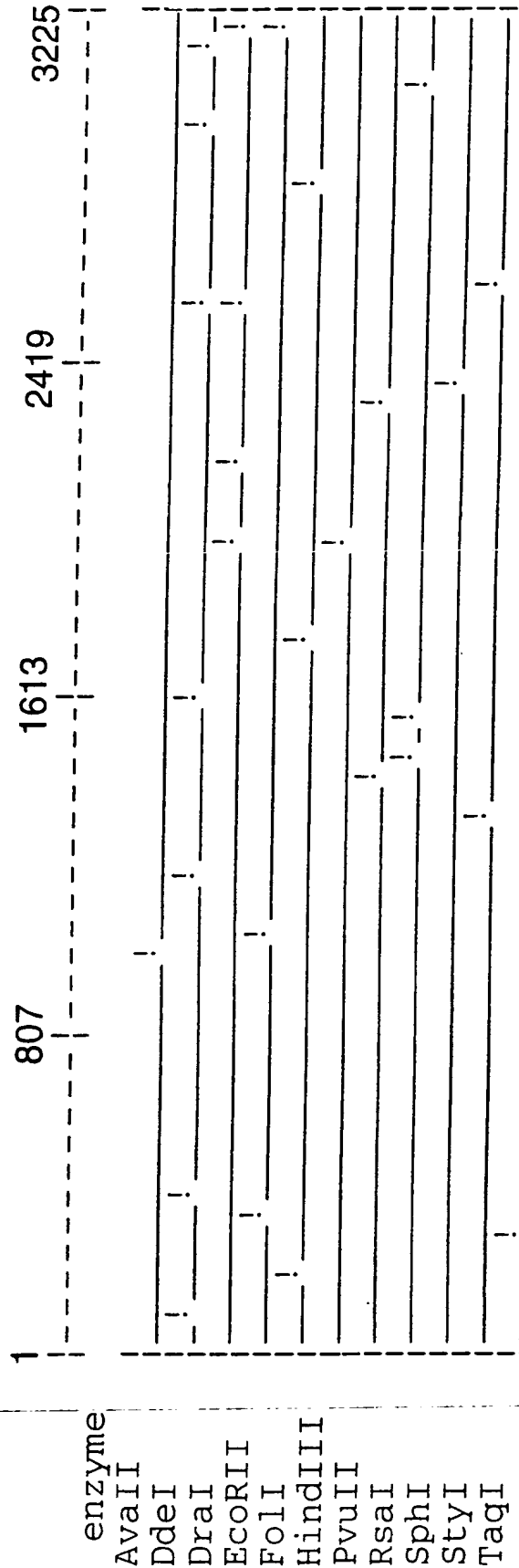


FIG.3

APPROVED	O.G. FIG.	
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650790-8294160

*M. catarrhalis* 4223 *tbpB* gene

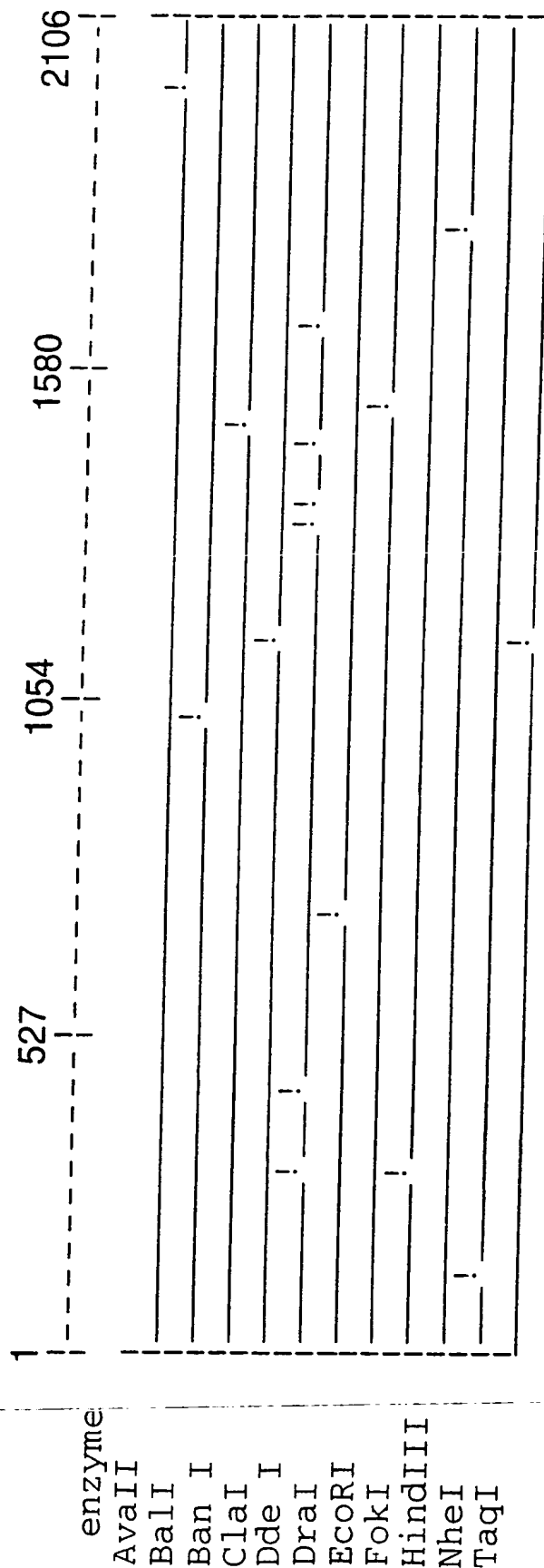


FIG.4

APPROVED	O.G. FIG.	
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FIG. 5A

Sequence of *M. catarrhalis* 4223 *tbpA* gene

TATTTTGACAAGCTATACACTAAATCAAAAATTAATCACTTTGGTTGGTGGTTTAGCAAGCAAAATGGT  
TATTTTGGTAAACAATTAAAGTTCCTTAAACGATACACGCTCATAAACAGATGGTTTTTGGCATCTGCAAT  
TTGATGCCCTGCCCTTGATTTGGTTGGGTGATCGGTGATCAAAAGTGCAAAAGCCAAACAGGTGGTCATTG  
ATG AAT CAA TCA AAA CAA AAC AAC AAA TCC AAA AAA TCC AAA CAA GTA TTA AAA 54  
MET Asn Gln Ser Lys Lys Gln Asn Asn Lys Ser Lys Lys Ser Lys Gln Val Leu Lys  
CTT AGT GCC TTG TCT TTG GGT CTG CTT AAC ATC ACG CAG GTG GCA CTG GCA AAC 108  
Leu Ser Ala Leu Ser Leu Gly Leu Leu Asn Ile Thr Gln Val Ala Leu Ala Asn  
ACA ACG GCC GAT AAG GCG GAG GCA ACA GAT AAG ACA AAC AAC CTT GTT GTT GTC TTG 162  
Thr Thr Ala Asp Lys Lys Ala Glu Ala Thr Asp Lys Thr Asn Leu Val Val Leu  
GAT GAA ACT GTT GTA ACA GCG AAG AAA AAC GCC CGT AAA GCC AAC GAA GTT ACA 216  
Asp Glu Thr Val Val Thr Ala Lys Lys Asn Ala Arg Lys Ala Asn Glu Val Thr

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650130-82924160

FIG.5B

GGG CTT	GGT AAG GTG GTC AAA ACT GCC	GAG ACC ATC AAT AAA GAA CAA GTG	270 CTA
Gly Leu	Gly Lys Val Val Lys Thr Ala	Glu Thr Ile Asn Lys Glu Gln Val	Leu
AAC ATT	CGA GAC TTA ACA CGC TAT GAC	CCT GGC ATT GCT GTG GTT GAG CAA	324 GGT
Asn Ile	Arg Asp Leu Thr Arg Tyr Asp	Pro Gly Ile Ala Val Val Glu Gln	Gly
CGT GGG	GCA AGC TCA GGC TAT TCT ATT	CGT GGT ATG GAT AAA AAT CCG GTG	378 GCG
Arg Gly	Ala Ser Gly Ser Tyr Tyr Ile	Arg Gly MET Asp Lys Asn Arg Val	Ala
GTA TTG	GTT GAT GGC ATC AAT CAA GCC	TAT GCC CTA CAA GGC CCT	432 GTG
Val Leu	Val Asp Val Ile Asn Gln Ala	Tyr Ala Leu Gln Gly Pro Val	
GCA GGC	AAA AAT TAT GCC GCA GGT GGG	GCA ATC AAC GAA ATA GAA TAC	486 AAT
Ala Gly	Lys Asn Tyr Ala Ala Gly Gly	Ile Asn Glu Ile Glu Tyr Glu	Asn
GTC CGC	TCC GTT GAG ATT AGT AAA GGT	GCA AAT TCA AGT GAA TAC GGC	540 TCT
Val Arg	Ser Val Glu Ile Ser Lys Gly	Ala Asn Ser Ser Glu Tyr Gly	GGG Ser Gly

APPROVED	O.G. FIG.	
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FIG.5C

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GCA TTA	TCT	GGC	TCT	GTG	GCA	TTT	GTT	ACC	AAA	ACC	GCC	GAT	GAC	ATC	ATC	AAA	594
Ala	Leu	Ser	Gly	Ser	Val	Ala	Phe	Val	Thr	Lys	Thr	Ala	Asp	Ile	Ile	Lys	
GAT GGT	AAA	GAT	TGG	GGC	GTG	CAG	ACC	AAA	ACC	GCC	TAT	GCC	AGT	AAA	AAT	AAC	648
Asp	Gly	Lys	Asp	Trp	Gly	Val	Gln	Thr	Lys	Thr	Ala	Tyr	Ala	Ser	Lys	Asn	
GCA TGG	GTT	AAT	TCT	GTG	GCA	GCA	GCA	GGC	AAG	GCA	GGT	TCT	TTT	AGC	GGT	CTT	702
Ala	Trp	Val	Asn	Ser	Val	Ala	Ala	Ala	Gly	Lys	Ala	Gly	Ser	Phe	Ser	Gly	
ATC ATC	TAC	ACC	GAC	CGC	CGT	GGT	CAA	GAA	TAC	AAG	GCA	CAT	GAT	GAT	GCC	TAT	756
Ile	Ile	Tyr	Thr	Asp	Arg	Arg	Gly	Gln	Glu	Tyr	Lys	Ala	His	Asp	Asp	Ala	
CAG GGT	AGC	CAA	AGT	TTT	GAT	AGA	GCG	GTG	GCA	ACC	ACT	GAC	CCA	AAT	AAC	CGA	810
Gln	Gly	Ser	Gln	Ser	Phe	Asp	Arg	Ala	Val	Ala	Thr	Thr	Asp	Pro	Asn	Arg	
ACA TTT	TTA	ATA	GCA	AAT	GAA	TGT	GCC	AAT	GGT	AAT	TAT	GAG	GCG	TGT	GCT	GCT	864
Thr	Phe	Leu	Ile	Ala	Asn	Glu	Cys	Ala	Asn	Gly	Asn	Tyr	Glu	Ala	Cys	Ala	
GGC GGT	CAA	ACC	AAA	CTT	CAA	GCC	AAG	CCA	ACC	AAT	GTG	CGT	GAT	AAG	GTC	AAT	918
Gly	Gly	Gln	Thr	Lys	Leu	Gln	Ala	Lys	Pro	Thr	Asn	Val	Arg	Asp	Lys	Val	

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FIG.5D

GTC Val	AAA Lys	GAT Asp	TAT Tyr	ACA Thr	GGT Gly	CCT Pro	AAC Asn	CGC Arg	CTT Leu	ATC Ile	CCA Pro	AAC Asn	CCA Pro	CTC Leu	ACC Thr	CAA Gln	GAC Asp	972
AGC Ser	AAA Lys	TCC Ser	TTA Leu	CTG Leu	CTT Leu	CGC Arg	CCA Pro	GGT Gly	TAT Tyr	CAG Gln	CTA Leu	AAC Asn	GAT Asp	AAG Lys	CAC His	TAT Tyr	GTC Val	1026
GGT Gly	GGT Gly	GTG Val	TAT Tyr	GAA Glu	ATC Ile	ACC Thr	AAA Lys	CAA Gln	AAC Asn	TAC Tyr	GCC Ala	ATG MET	CAA Gln	GAT Asp	AAA Lys	ACC Thr	GTG Val	1080
CCT Pro	GCT Ala	TAT Tyr	CTG Leu	ACG Thr	GTT Val	CAT His	GAC Asp	ATT Ile	GAA Glu	AAA Lys	TCA Ser	AGG Arg	CTC Leu	AGC Ser	AAC Asn	CAT His	GCC Ala	1134
CAA Gln	GCC Ala	AAT Asn	GGC Gly	TAT Tyr	TAT Tyr	CAA Gln	GGC Gly	ASN Asn	AAT Asn	CTT Leu	GGT Gly	GAA Glu	CGC Arg	ATT Ile	CGT Arg	GAT Asp	ACC Thr	1188
ATT Ile	GGG Gly	CCA Pro	GAT Asp	TCA Ser	GGT Gly	TAT Tyr	GGC Gly	ATC Ile	AAC Asn	TAT Tyr	GCT Ala	CAT His	GGC Gly	GTA Val	TTT Phe	TAT Tyr	GAT Asp	1242

APPROVED	O.G. FIG.	
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APPROVED	O.G.FIG.	
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## FIG.5E

1269	GAA AAA CAC CAA AAA GAC CGC CTA GGG CTT GAA TAT GTT TAT GAC AGC AAA GGT	1296	Glu Lys His Gln Lys Asp Arg Leu Gly Leu Glu Tyr Val Tyr Asp Ser Lys Gly
1323	GAA AAT AAA TGG TTT GAT GAT GTG CGT GTG TCT TAT GAT AAG CAA GAC ATT ACG	1350	Glu Asn Lys Lys Trp Phe Asp Asp Val Arg Val Ser Tyr Asp Lys Gln Asp Ile Thr
1377	CTA CGC AGC CAG CAG CTG ACC AAC ACG CAC TGT TCA ACC TAT CCG CAC ATT GAC AAA	1404	Leu Arg Ser Gln Leu Thr Asn Thr His Cys Ser Thr Tyr Pro His Ile Asp Lys
1431	AAT TGT ACG CCT GAT GTC AAT AAA CCT TTT TCG GTA AAA GAG GTG GAT AAC AAT	1458	Asn Cys Thr Pro Asp Val Asn Lys Pro Phe Ser Val Lys Glu Val Asp Asn Asn
1485	GCC TAC AAA GAA CAG CAC AAT TTA ATC AAA GCC GTC TTT AAC AAA ATG GCG	1512	Ala Tyr Lys Glu Gln His Asn Leu Ile Lys Ala Val Phe Asn Lys Lys MET Ala
1539	TTG GGC AGT ACG CAT CAT CAC ATC ATC AAC CTG CAA GTT GGC TAT GAT AAA TTC AAT	1566	Leu Gly Ser Thr His His His Gln His Ile Asn Leu Gln Val Gly Tyr Asp Lys Phe Asn
1593	TCA AGC CTG AGC CGT GAA GAT TAT CGT TTG GCA ACC CAT CAG TCT TAT CAA AAA	1620	Ser Ser Leu Ser Arg Glu Asp Tyr Arg Leu Ala Thr His Gln Ser Tyr Gln Lys

**SUBSTITUTE SHEET (RULE 26)**

CTT GAT Leu Asp	TAC Tyr	ACC Thr	CCA Pro	CCA Pro	AGT Ser	AAC Asn	CCT Pro	TTG Leu	CCA Pro	GAT Asp	AAG Lys	TTT Phe	AAG Lys	CCC Pro	ATT Ile	TTA Leu	1674
GGT TCA Gly Ser	AAC Asn	AAC Asn	AAA Lys	CCC Pro	ATT Ile	TGC Cys	CTT Leu	GAT Asp	GCT Ala	TAT Tyr	GGT Gly	TAT Tyr	GGT Gly	CAT His	GAC Asp	CAT His	1728
CCA CAG Pro Gln	GCT Ala	TGT Cys	AAC Asn	GCC Ala	AAA Lys	AAC Asn	AGC Ser	ACT Thr	TAT Tyr	CAA Gln	AAT Asn	TTT Phe	GCC Ala	ATC Ile	AAA Lys	AAA Lys	1782
GGC ATA Gly Ile	GAG Glu	CAA Gln	TAC Tyr	AAC Asn	CAA Gln	AAA Lys	ACC Thr	AAT Asn	ACC Thr	GAT Asp	AAG Lys	ATT Ile	GAT Asp	TAT Tyr	CAA Gln	GCC Ala	1836
ATC ATT Ile Ile	GAC Asp	CAA Gln	TAT Tyr	GAT Asp	AAA Lys	CAA Gln	Asn Asn	CCC Pro	AAC Ser	AGC Ser	ACC Thr	CTA Leu	AAA Lys	CCC Pro	TTT Phe	GAG Glu	1890
AAA ATC Lys Ile	AAA Lys	CAA Gln	AGT Ser	TTG Leu	GGG Gly	CAA Gln	GAA Glu	AAA Lys	TAC Tyr	AAC Asn	AAG Lys	ATA Ile	GAC Asp	GAA Glu	CTT Leu	GGC Gly	1944

APPROVED	O.G. FIG.	
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## FIG.5G

TTT AAA GCT TAT AAA GAT TTA CGC AAC	1971	GAA TGG GCG GGT TGG ACT AAT GAC AAC	1998
Phe Lys Ala Tyr Lys Asp Leu Arg Asn Glu Trp Ala Gly Trp Thr Asn Asp Asn			
AGC CAA CAA AAT GCC AAT AAA GGC ACG	2025	GAT AAT ATC TAT CAG CCA AAT CAA GCA	2052
Ser Gln Gln Asn Ala Asn Lys Gly Thr		Ile Tyr Gln Pro Asn Gln Ala	
ACT GTG GTC AAA GAT GAC AAA TGT AAA	2079	TAT AGC GAG ACC AAC AGC TAT GCT GAT	2106
Thr Val Val Lys Asp Asp Lys Cys Lys		Tyr Ser Glu Thr Asn Ser Tyr Ala Asp	
TGC TCA ACC ACT CGC CAC ATC ATC AGT GGT	2133	GAT AAT TAT TTC ATC GCT TTA AAA GAC	2160
Cys Ser Thr Thr Arg His Ile Ser Gly		Asn Tyr Phe Ile Ala Leu Lys Asp	
AAC ATC ACC ATC AAT AAA TAT GTT GAT	2187	TTG GGG CTG GGT GCT CGC TAT GAC AGA	2214
Asn MET Thr Ile Asn Lys Tyr Val Asp		Leu Gly Ala Arg Tyr Asp Arg	
ATC AAA CAC AAA TCT GAT GTG CCT TTG	2241	GTA GAC AAC AGT GCC AGC AAC CAG CTG	2268
Ile Lys His Lys Ser Asp Val Pro Leu		Val Asp Asn Ser Ala Ser Asn Gln Leu	

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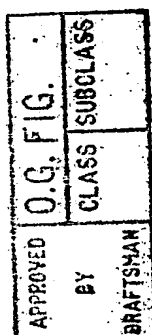
660550-8292460

## FIG.5H

TCT TGG	AAT TTT	GGC GTG	GTC GTC	AAG CCC	ACC AAT	TGG CTG	GAC ATC	GCT TAT	2322
Ser Trp	Asn Phe	Gly Val	Val Val	Lys Val	Thr Asn	Trp Leu	Asp Ile	Ala Tyr	
AGA AGC	TCG CAA	GGC TTT	CGC ATG	CCA AGT	TTT TCT	GAA ATG	TAT GGC	GAA CGC	2376
Arg Ser	Ser Gln	Gly Phe	Arg MET	Pro Ser	Phe Ser	Glu MET	Tyr Gly	Glu Arg	
TTT GGC	GTA ACC	ATC GGT	AAA GGC	ACG CAA	CAT GGC	TGT AAG	GGT CTT	TAT TAC	2430
Phe Gly	Val Thr	Ile Gly	Lys Lys	Thr Thr	Gln His	Cys Lys	Gly Leu	Tyr Tyr	
ATT TGT	CAG CAG	ACT GTC	CAT CAT	ACC AAG	CTA AAA	CCT GAA	AAA TCC	TTT AAC	2484
Ile Cys	Gln Gln	Thr Val	His His	Thr Thr	Lys Leu	Pro Glu	Lys Ser	Phe Asn	
CAA GAA	ATC GGA	GCG ACT	TTA CAT	AAC CAC	TTA GGC	AGT AGT	GAG GTT	AGT TAT	2538
Gln Glu	Ile Gly	Ala Thr	Leu Leu	His Asn	Gly Gly	Ser Leu	Glu Val	Ser Tyr	
TTT AAA	AAT CGC	TAT ACC	GAT TTT	ATT GTT	GGT AAA	AGT AGT	GAG ATT	AGA ACC	2592
Phe Lys	Asn Arg	Tyr Thr	Asp Leu	Ile Ile	Gly Lys	Ser Ser	Glu Ile	Arg Thr	
CTA ACC	CAA GGT	GAT AAT	GCA GGC	AAA CAG	CGT GGT	AAA GGT	GAT TTG	GGC TTT	2646
Leu Thr	Gln Gly	Asp Asn	Ala Gly	Lys Lys	Arg Gly	Lys Gly	Asp Leu	Gly Phe	

FIG.51

CAT AAT	GGA CAA GAT GCT GAT TTG ACA GGC ATT AAC ATT CTT GGC AGA CTT GAC	2673	2700
His Asn	Gly Gln Asp Ala Asp Leu Thr Gly Ile Asn Ile Leu Gly Arg Leu Asp		
CTA AAC	GCT GTC AAT AGT CGC CTT CCC TAT GGA TTA TAC TCA ACA CTG GCT TAT	2727	2754
Leu Asn	Ala Val Asn Ser Arg Leu Pro Tyr Gly Leu Tyr Ser Thr Leu Ala Tyr		
AAC AAA	GTT GAT GAT AAA GGA AAA ACC TTA AAC CCA ACT TTG GCA GGA ACA AAC	2781	2808
Asn Lys	Val Asp Val Lys Lys Gly Lys Thr Leu Asn Pro Thr Leu Ala Gly Thr Asn		
ATA CTG	TTT GAT GCC ATC CAG CCA TCT CGT TAT GTG GTG GGG CTT GGC TAT GAT	2835	2862
Ile Leu	Phe Asp Ala Ile Gln Pro Ser Arg Tyr Val Val Gly Leu Gly Tyr Asp		
GCC CCA	AGC CAA AAA TGG GGA GCA AAC GCC ATA TTT ACC CAT TCT GAT GCC AAA	2889	2916
Ala Pro	Ser Gln Lys Trp Gly Ala Asn Ala Ile Phe Thr His Ser Asp Ala Lys		
AAT CCA	AGC GAG CTT TTG GCA GAT AAG AAC TTA GGT AAT GGC AAC ATT CAA ACA	2943	2970
Asn Pro	Ser Glu Leu Leu Ala Asp Lys Asn Gly Asn Gly Asn Ile Gln Thr		



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FIG.5J

2997  
 AAA CAA GCC ACC AAA GCA AAA TCC ACG CCG TGG CAA ACA CTT GAT TTG TCA GGT  
 Lys Gln Ala Thr Lys Ala Lys Ser Thr Pro Trp Gln Thr Leu Asp Leu Ser Gly

3051  
 TAT GTA AAC ATA AAA GAT AAT TTT ACC TTG CGT GCT GGC GCA GGT GTA TTT  
 Tyr Val Asn Ile Lys Asp Asn Phe Thr Leu Arg Ala Gly Val Tyr Asn Val Phe

3105  
 AAT ACC TAT TAC ACC ACT TGG GAG GCT TTA CGC CAA ACA GCA GAA GGG GCG GTC  
 Asn Thr Tyr Tyr Thr Thr Trp Glu Ala Leu Arg Gln Thr Ala Glu Gly Ala Val

3159  
 AAT CAG CAT ACA GGA CTG AGC CAA GAT AAG CAT TAT GGT CGC TAT GCC GCT CCT  
 Asn Gln His Thr Gly Leu Ser Gln Asp Lys His Tyr Gly Arg Tyr Ala Ala Pro

3213  
 GGA CGC AAT TAC CAA TTG GCA CTT GAA ATG AAG TTT TAA  
 Gly Arg Asn Tyr Gln Leu Ala Leu Glu MET Lys Phe

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG.6A

Sequence of *M. catarrhalis* 4223 *tbpB* gene

GTAAATTGCGGTATTTGTGCTATCATAAATGCATTATCAAAATGCTCAAAATAACGCCAAATGCACAT

TGTCAGCATGCCAAATAGGCATCAACAGACTTTTTTTAGATAATACCATCAACCCATCAGAGGATTATTTT

27 54

ATG AAA CAC ATT CCT TTA ACC ACA CTG TGT GTG GCA ATC TCT GCC GTC TTA TTA

MET Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val Leu Leu

81 108

ACC GCT TGT GGT GGC AGT GGT GGT TCA AAT CCA CCT GCT CCT ACG CCC ATT CCA

Thr Ala Cys Gly Gly Ser Gly Gly Thr Thr Gly Asn Pro Pro Ala Pro Thr Pro Ile Pro

135 162

AAT GCT AGC GGT TCA GGT AAT ACT GGT AAC ACT GGT AAT GCT GGT GGT ACT GAT

Asn Ala Ser Gly Ser Thr Thr Thr Gly Asn Thr Thr Gly Asn Ala Gly Gly Thr Asp

189 216

AAT ACA GCC AAT GCA GGT AAT ACA GGC GGT ACA AAC TCT GGT ACA GGC AGT GCC

Asn Thr Ala Asn Ala Gly Asn Thr Thr Gly Gly Thr Asn Ser Gly Thr Gly Ser Ala

243 270

AAC ACA CCA GAG CCA AAA TAT CAA GAT GTA CCA ACT GAG AAA AAT GAA AAA GAT

Asn Thr Pro Glu Pro Lys Tyr Gln Asp Val Pro Thr Thr Glu Lys Asn Glu Lys Asp

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AAA GTT	TCA TCC ATT CAA GAA CCT GCC	ATG GGT TAT GGC ATG GCT TTG AGT	324
Lys Val	Ser Ser Ile Gln Glu Pro Ala	MET Gly Tyr Gly MET Ala Leu Ser	Lys
ATT AAT	CTA CAC AAC CGA CAA GAC ACG	CAA TTA GAT GAA AAA AAT ATC ATT	378
Ile Asn	Leu His Asn Arg Gln Asp Thr	Pro Leu Asp Glu Lys Asn Ile Ile Thr	ACC
TTA GAC	GGT AAA AAA CAA GTT GCA GAA	GGT AAA AAA TCG CCA TTG CCA TTT	432
Leu Asp	Gly Lys Lys Gln Val Ala Glu	Gly Lys Ser Pro Leu Pro Phe Ser	TCG
TTA GAT	GTA GAA AAT AAA TTG CTT GAT	GGC TAT ATA GCA AAA ATG AAT GTA	486
Leu Asp	Val Glu Asn Lys Lys Leu Leu Asp	Gly Tyr Ile Ala Lys MET Asn Val Ala	CGC
GAT AAA	AAT GCC ATT GGT GAC AGA ATT	AAG AAA GGT AAT AAA GAA ATC TCC	540
Asp Lys	Asn Ala Ile Gly Asp Arg Ile	Lys Lys Gly Asn Lys Glu Ile Ser	Asp
GAA GAA	CTT GCC AAA CAA ATC AAA GAA	GCT GTG CGT AAA AGC CAT GAG TTT	594
Glu Glu	Leu Ala Lys Gln Ile Lys Glu	Ala Val Arg Lys Ser His Glu Phe	Gln



FIG.6C

APPROVED.	O.G. FIG.
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CAA Gln	GTA Val	TTA TCA TCA CTG GAA AAC AAA	ATT TTT CAT TCA AAT GAC GGA ACA ACC	648
AAA Lys	GCA Ala	ACC ACA CGA GAT TTA AAA TAT	GTT GAT TAT GGT TAC TAC TTG GCG AAT	702
GAT Asp	GGC Gly	AAT Asn Tyr Leu Thr Val Lys	ACA Thr Tyr Arg Asp Leu Lys	729
GGT Gly	GGT Gly	GTG Val Phe Tyr TAT TTT	GTT TAT GAT GGT TAC TAC TTA GGC CCT GTG	756
GCG Ala	GTC Val	AAA Thr Asn Tyr Leu Thr Thr	ACA Thr Val Lys Thr Thr	783
AAC Asn	CGA Thr	AGC Thr Lys Glu His Trp Asp	ACC Thr Ala Lys Thr Thr	837
AAC Asn	CGA Thr	AGC Thr Lys Glu His Trp Asp	ACC Thr Ala Lys Thr Thr	864
AAC Asn	CGA Thr	AGC Thr Lys Glu His Trp Asp	ACC Thr Ala Lys Thr Thr	918

APPROVED	O.G. FIG.	
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FIG.6D

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TCT	TCA	AAA	GAT	GAA	TAC	AAC	CGC	TTA	TTA	ACT	AAA	GAA	GAC	TCT	GCC	CCT	GAT	972
Ser	Ser	Lys	Asp	Glu	Tyr	Asn	Arg	Leu	Leu	Thr	Lys	Glu	Asp	Ser	Ala	Pro	Asp	
GGT	CAT	AGC	GGT	GAA	TAT	GGC	CAT	AGC	AGT	GAG	TTT	ACT	GTT	AAT	TTT	AAG	GAA	1026
Gly	His	Ser	Gly	Glu	Tyr	Gly	His	Ser	Ser	Glu	Phe	Thr	Val	Asn	Phe	Lys	Glu	
AAA	AAA	TTA	ACA	GGT	AAG	CTG	TTT	AGT	AAC	CTA	CAA	GAC	CGC	CAT	AAG	GGC	AAT	1080
Lys	Lys	Leu	Thr	Gly	Lys	Leu	Phe	Ser	Asn	Leu	Gln	Asp	Arg	His	Lys	Gly	Asn	
GTT	ACA	AAA	ACC	GAA	CGC	TAT	GAC	ATC	GAT	GCC	AAT	ATC	CAC	GGC	AAC	CGC	TTC	1134
Val	Thr	Lys	Thr	Glu	Arg	Tyr	Asp	Ile	Asp	Ala	Asn	Ile	His	Gly	Asn	Arg	Phe	
CGT	GGC	AGT	GCC	ACC	GCA	AGC	AAT	AAA	AAT	GAC	ACA	AGC	AAA	CAC	CCC	TTT	ACC	1188
Arg	Gly	Ser	Ala	Thr	Ala	Ser	Asn	Lys	Asn	Asp	Thr	Ser	Lys	His	Pro	Phe	Thr	
AGT	GAT	GCC	AAC	AAT	AGG	CTA	GAA	GGT	GGT	TTT	TAT	GGG	CCA	AAA	GGC	GAG	GAG	1242
Ser	Asp	Ala	Asn	Asn	Arg	Leu	Glu	Gly	Gly	Phe	Tyr	Gly	Pro	Lys	Gly	Glu	Glu	

APPROVED	O.G. FIG.	
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FIG.6E

CTG GCA	GGT AAA	TTC TTA	ACC AAC	AAA CTC	TTT GGC	GTC TTT	GGT GCT	1296
Leu Ala	Gly Lys	Phe Leu	Thr Asn	Asp Asn	Lys Leu	Phe Gly	Val Phe	Gly Ala
AAA CGA	GAG AGT	AAA GCT	GAG GAA	AAA ACC	GAA GCC	ATC TTA	GAT GCC	TAT GCA
Lys Arg	Glu Ser	Lys Ala	Glu Glu	Lys Thr	Glu Ala	Ile Leu	Asp Ala	Tyr Ala
CTT GGC	ACA TTT	AAT AAC	AGT AAC	GCA ACC	ACA TTC	ACC ACC	TTT ACC	GAA AAA
Leu Gly	Thr Phe	Asn Thr	Ser Asn	Ala Thr	Thr Phe	Thr Pro	Phe Thr	Glu Lys
CAA CTC	GAT AAC	TTT GGC	AAT AAC	GCC AAA	AAA TTG	GTC TTA	GGT TCT	ACC GTC
Gln Leu	Asp Asn	Phe Gly	Asn Ala	Lys Ala	Lys Leu	Val Leu	Gly Ser	Thr Val
								Ile
GAT TTG	GTG CCT	ACT ACT	GAT GCC	ACC AAC	AAA GAC	AAG CCA	GAG	1512
Asp Leu	Val Pro	Thr Thr	Asp Ala	Thr Lys	Asn Glu	Thr Lys	Asp Lys	Pro Glu
TCT GCC	ACA AAC	GAA GCG	GAG GGC	ACT TTG	ATG GTG	AAT GAT	GAA GTT	AGC GTC
Ser Ala	Thr Asn	Glu Ala	Gly Glu	Thr Leu	<u>MET Val</u>	<u>Asn Asp</u>	<u>Glu Val</u>	<u>Ser Val</u>
								1566

FIG.6F

AAA ACC	TAT	GCC	AAA	AAC	TTT	GAA	TAC	CTA	AAA	TTT	GGT	GAG	CTT	AGT	ATC	GGT	1620
Lys Thr	Tyr	Gly	Lys	Asn	Phe	Glu	Tyr	Leu	Lys	Phe	Gly	Glu	Leu	Ser	Ile	Gly	
GGT AGC	CAT	AGC	GTC	TTT	TTA	CAA	GCC	GAA	CGC	ACC	GCT	ACC	ACA	GGC	GAG	AAA	1674
Gly Ser	His	Ser	Val	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Ala	Thr	Thr	Gly	Glu	Lys	
GCC GTA	CCA	ACC	ACA	GCC	ACA	GCC	AAA	TAT	TTG	GGG	AAC	TGG	GTA	GGA	TAC	ATC	1728
Ala Val	Pro	Thr	Thr	Gly	Thr	Ala	Lys	Tyr	Leu	Gly	Asn	Trp	Val	Gly	Tyr	Ile	
ACA GGA	AAG	GAC	ACA	GGA	ACG	GCC	ACA	GGA	AAA	AGC	TTT	ACC	GAT	GCC	CAA	GAT	1782
Thr Gly	Lys	Asp	Thr	Gly	Thr	Gly	Thr	Gly	Lys	Ser	Phe	Thr	Asp	Ala	Gln	Asp	
GTT GCT	GAT	TTT	GAC	ATT	GAT	TTT	GGA	AAT	AAA	TCA	GTC	AGC	GGT	AAA	CTT	ATC	1836
Val Ala	Asp	Phe	Asp	Ile	Asp	Phe	Gly	Asn	Lys	Ser	Val	Ser	Gly	Lys	Leu	Ile	
ACC AAA	GGC	CGC	CAA	GAC	CCT	GTA	TTT	AGC	ATC	ACA	GGT	CAA	ATC	GCA	GGC	AAT	1890
Thr Lys	Gly	Arg	Gln	Asp	Pro	Val	Phe	Ser	Ile	Thr	Gly	Gln	Ile	Ala	Gly	Asn	

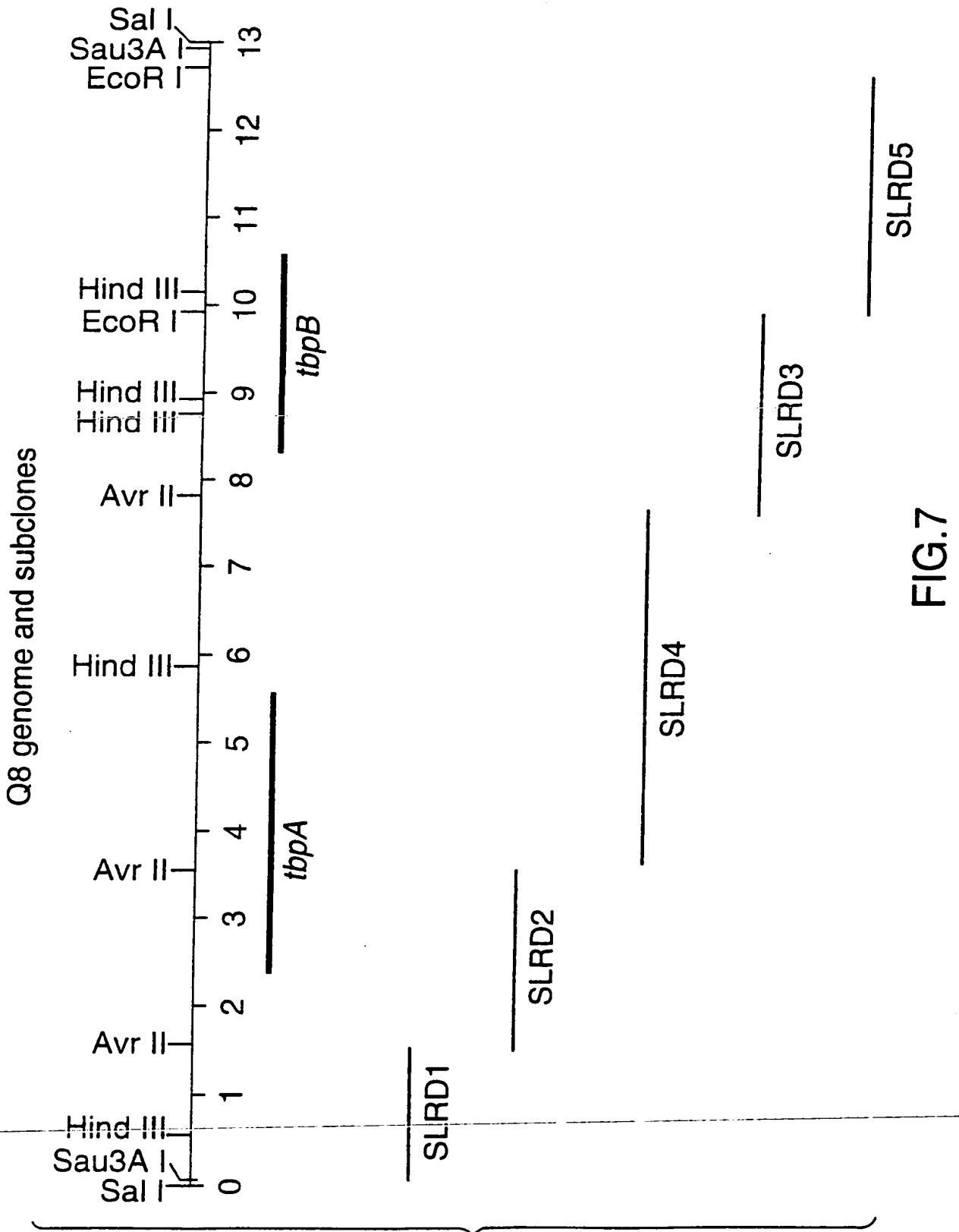
APPROVED	O.G.FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 6G

GGC TGG	ACA GGG	ACA GGC	AGC ACC	ACC ACC	AAA GCG	GAC GCA	GGA GGC	TAC AAG	ATA	1944
Gly Trp	Thr Gly	Thr Ala	Ser Thr	Thr Thr	Lys Ala	Asp Ala	Gly Gly	Tyr Tyr	Lys Ile	
GAT TCT	AGC AGT	ACA GGC	AAA TCC	ATC ATC	GCC ATC	AAA GAT	GCC AAT	GTT ACA	GGG	1998
Asp Ser	Ser Ser	Thr Thr	Lys Lys	Ser Ile	Ala Ile	Lys Asp	Ala Asn	Val Thr	Gly	
GGC TTT	TAT GGT	CCA AAT	GCA AAC	GAG GAG	ATG GGC	GGG TCA	TTT ACA	CAC AAC	GCC	2052
Gly Phe	Tyr Gly	Pro Asn	Ala Ala	Asn Glu	MET Gly	Gly Ser	Phe Thr	His Asn	Ala	
GAT GAC	AGC AAA	GCC TCT	GTG GTC	TTT TTT	GGC ACA	AAA AGA	CAA CAA	GAA GTT	AAG	2106
Asp Asp	Ser Lys	Ala Ser	Val Val	Phe Phe	Gly Thr	Lys Arg	Gln Gln	Glu Val	Lys	

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

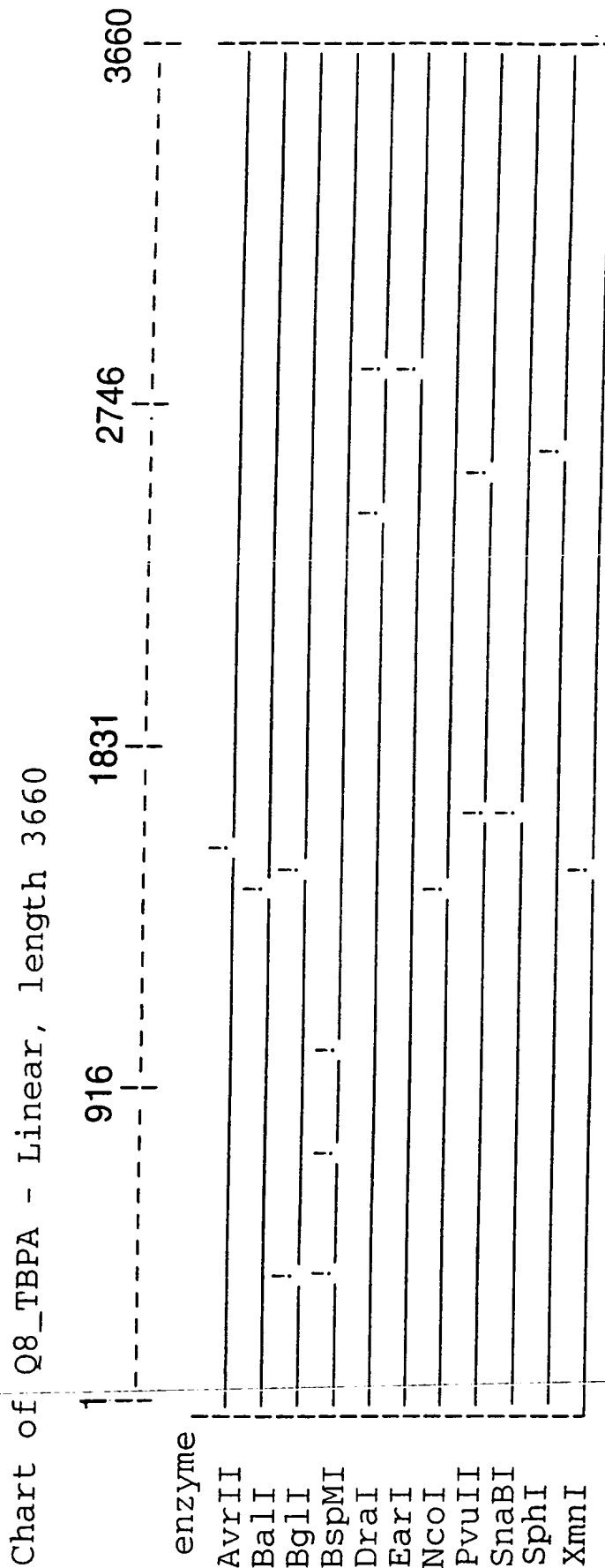


FIG.8

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660790-82924760

Chart of Q8\_TBPB\_SLRD3\_SLRD5 - Linear, length 3487

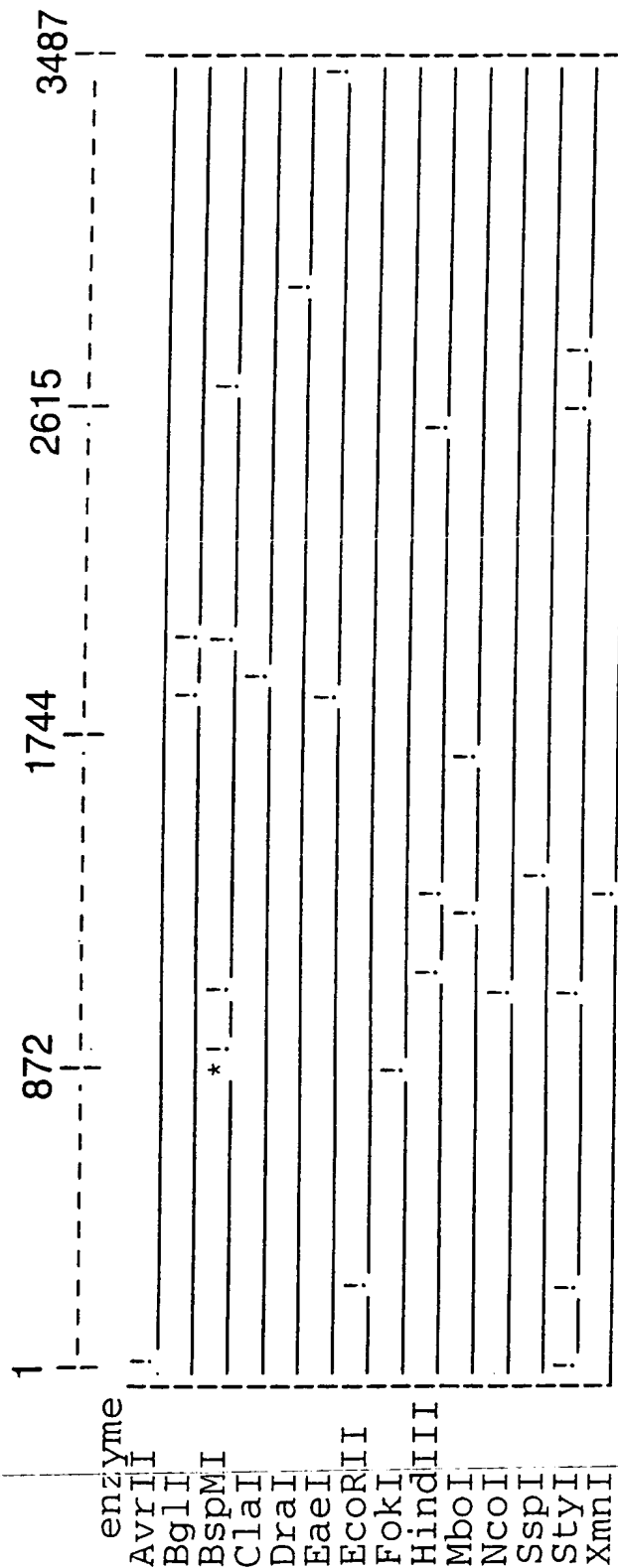


FIG.9



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

[illegible]

FIG. 10A

Q8 tbpA gene sequence

A A T G A T A C A A A T G G T T G T A T T A T C A C T  
 10 20 30  
 T G T A T T G T A T T A A T T T A C T T A T T T T  
 40 50 60

ACAAAC TATACACTAAATCAAAATTAA T  
70 80 90  
CACTTGGTTGGTGGTTTAGCAAGCAAA  
100 110 120

TGGTTATT TTTGGTAAACAATT AAGTCTTA  
130 140 150  
A A A C G A T A C A C G C T C A T A A C A G A T G G T T  
160 170 180

TTGGCA TCTTCAATTGATGCCCTTG 200  
210  
TGATTGGTTGGGGTGTTGATGTATCCA 220  
230  
240

AGTACAAAGCCACAGGTGGTCA TTGATG  
250 260 270  
MET

APPROVED	06.FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG.10B

WO 97/32980

26/90

09/142628

PCT/CA97/00163

ASN GLN SER LYS LYS SER LYS SER LYS  
AATCAATCCAAATAATCCAAATCCAA  
280 290 300

GLN VAL LEU LYS LEU SER ALA LEU SER LEU  
CAAGTATTAAACTTAGTGCCCTTGCTTG  
310 320 330

GLY LEU LEU ASN ILE THR GLN VAL ALA LEU  
GGCTGCTTAACATCACGCAGGTGGCACTG  
340 350 360

ALA ASN THR THR ALA ASP LYS ALA GLU ALA  
GCAACACACGGCCGATAGGCGGAGGCA  
370 380 390

THR ASP LYS THR ASN LEU VAL VAL VAL LEU  
ACAGATAAGACAAACCTTGTTGTCTCTTG  
400 410 420

ASP GLU THR VAL VAL THR ALA LYS ASN  
GATGAACCTGTGTACAGCGAAGAAAC  
430 440 450

ALA ARG LYS ALA ASN GLU VAL THR GLY LEU  
GCCCGTAAGCCCAACGAAGTTACAGGGCTT  
460 470 480

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

600F50" 32980

FIG.10C

```

GLY  LYS  VAL  LYS  THR  ALA  GLU  THR  ILE
GGTAAGGTGGTCAAAACTGCCGAGACCATC
490
ASN  LYS  GLU  VAL  LEU  ASN  ILE  ARG  ASP
AATAAGAACAGTGCTAAACATTTCGAGAC
520
LEU  THR  ARG  TYR  ASP  PRO  GLY  ILE  ALA  VAL
TTAACACGCTATGACCCCTGGCATTTGCTGTG
550
VAL  GLU  GLN  GLY  ARG  GLY  ALA  SER  SER  GLY
GTGAGCAAGGTCGTGGGCAAGCTCAGGC
580
TYR  SER  ILE  ARG  GLY  MET  ASP  LYS  ASN  ARG
TATTCATAATCGTGATGGAATAAATCGT
610
VAL  ALA  VAL  LEU  VAL  ASP  GLY  ILE  ASN  GLN
GTGGCGGTATTGGTTGATGGCATCAATCAA
640
ALA  GLN  HIS  TYR  ALA  LEU  GLN  PRO  VAL
GCCAGCACTATGCCCTACAAGGCCCTGTG
670

```

FIG. 10D

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

```

ASP  ILE  ILE  LYS  LYS  ASP  GLY  TRP  GLY
GACATCATCAAGATGGTAAAGATTGGGCGC
850
860
870
880
890
900

```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

650150-32980

FIG.10E

```

ASN  ASN  ALA  TRP  VAL  ASN  SER  VAL  ALA  ALA
AATAACGCATGGGTTAATTCTGTGGCAGCA      910
                                     920
                                     930
                                     ALA  GLY  LYS  ALA  GLY  SER  PHE  SER  GLY  LEU
                                     GCAGGCAAGGCAGGTCTTTTAGCGGCTCTT      940
                                     950
                                     960

ILE  ILE  TYR  THR  ASP  ARG  ARG  GLY  GLN  GLU
ATCATCTACCCGACCGCCGTTGGTCAAGAA      970
                                     980
                                     990
                                     TYR  LYS  ALA  HIS  ASP  ASP  ALA  TYR  GLN  GLY
                                     TACAAGGCACATGATGATGCCCTATCAGGGT      1000
                                     1010
                                     1020

SER  GLN  SER  PHE  ASP  ARG  ALA  VAL  ALA  THR
AGCCAAAGTTTGTATAGAGCGGTGGCAACC      1030
                                     1040
                                     1050
                                     THR  ASP  PRO  ASN  ASN  PRO  LYS  PHE  LEU  ILE
                                     ACTGACCCAAATAACCCAAATAATTTTATAATA      1060
                                     1070
                                     1080

ALA  ASN  GLU  CYS  ALA  ASN  GLY  ASN  TYR  GLU
GCAATAATGATGTGCCCAATGGTAATTATGAG      1090
                                     1100
                                     1110

```

APPROVED	0:G.FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

FIG.10F

WO 97/32980

30/90

09/142628

PCT/CA97/00163

ALA CYS ALA ALA GLY GLY THR LYS LEU  
GCGTGCTGCTGCGGTCAACCAACTC  
1120 1130 1140

GLN ALA LYS PRO THR ASN VAL ARG ASP LYS  
CAGCTAAGCCCAACCAATGTGCTGATAAG  
1150 1160 1170

VAL ASN VAL LYS ASP TYR THR GLY PRO ASN  
GTCAATGTCAAGATTATACAGGTCCTAAC  
1180 1190 1200

ARG LEU ILE PRO ASN PRO LEU THR GIN ASP  
CGCCTTATCCCAACCCACTCACCCAGAC  
1210 1220 1230

SER LYS SER LEU LEU ARG PRO GLY TYR  
AGCAATCCCTTACTGCTTCGCCCAAGTTAT  
1240 1250 1260

GLN LEU ASN ASP LYS HIS TYR VAL GLY GLY  
CAGCTAACGATAAGCACTATGTCGGTGGT  
1270 1280 1290

VAL TYR GLU ILE THR LYS GIN ASN TYR ALA  
GTGTATGAATAACCAACAACACTACGCC  
1300 1310 1320

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660150" 82524160

FIG.10G

```

MET  GLN  ASP  LYS  THR  VAL  PRO  ALA  TYR  LEU
A T G C A A G A T A A A C C G T G C C T T A T C T G
1330
1340
      THR  VAL  HIS  ASP  ILE  GLU  LYS  SER  ARG  LEU
      A C G G T T C A T G A C A T T G A A A A T C A A G G C T C
1350
1360
SER  ASN  HIS  GLY  GLN  ALA  ASN  GLY  TYR  TYR
A G C A A C A T G G C C A A G C C A A T G G C T A T T A T
1390
1400
      GLN  GLY  ASN  ASN  LEU  GLY  GLU  ARG  ILE  ARG
      C A A G G C A A T A A C C T T G G T G A A C G C A T T C G T
1410
1420
ASP  ALA  ILE  GLY  ALA  ASN  SER  GLY  TYR  GLY
G A T G C C A T T G G G G C A A A T T C A G G T T A T G G C
1450
1460
      ILE  ASN  TYR  ALA  HIS  GLY  VAL  PHE  TYR  ASP
      A T C A A C T A T G C T C A T G G C G T A T T T A T G A C
1470
1480
GLU  LYS  HIS  GLN  LYS  ASP  ARG  LEU  GLY  LEU
G A A A A C A C C C A A A A G A C C G C C T A G G G C T T
1510
1520
1530

```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

6001500-82524150

FIG.10H

GLU TYR VAL TYR ASP SER LYS GLY GLU ASN  
G A A T A T G T T T A T G A C A G C A A A G G T G A A A T  
1540 1550 1560

LYS TRP PHE ASP ASP VAL ARG VAL SER TYR  
A A A T G G T T T G A T G A T G T G C G T G T G T C T T A T  
1570 1580 1590

ASP LYS GLN ASP ILE THR LEU ARG SER GLN  
G A C A A G C A A G A C A T T A C G C T A C G T A G C C A G  
1600 1610 1620

LEU THR ASN THR HIS CYS SER THR TYR PRO  
C T G A C C A A C A C G C A C T G T T C A A C C T A T C C G  
1630 1640 1650

HIS ILE ASP LYS ASN CYS THR PRO ASP VAL  
C A C A T T G A C A A A A A T T G T A C G C C T G A T G T C  
1660 1670 1680

ASN LYS PRO PHE SER VAL LYS GLU VAL ASP  
A A T A A A C C T T T T C G G T A A A G A G G T G G A T  
1690 1700 1710

ASN ASN ALA TYR LYS GLU GLN HIS ASN LEU  
A A C A A T G C C C T A C A A G A A C A G C A C A A T T A  
1720 1730 1740



/142628

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660490-8294160

FIG.10I

```

ILE LYS ALA VAL PHE ASN LYS LYS MET ALA
ATCAAAGCCGTCCTTAACAATAATGGCA
1750 1760 1770
LEU GLY ASN THR HIS HIS ILE ASN LEU
TTGGCAATACGCATCATCATCATCTG
1780 1790 1800

GLN VAL GLY TYR ASP LYS PHE ASN SER SER
CAGTTGGCTATGATAATAATTCAATCAGC
1810 1820 1830
LEU SER ARG GLU ASP TYR ARG LEU ALA THR
CTTAGCCGTGAAGATTATCGTTTGGCAACC
1840 1850 1860

HIS GLN SER TYR GLN LYS LEU ASP TYR THR
CATCAATCTTATCAAAACTTGATTACACC
1870 1880 1890
PRO PRO SER ASN PRO LEU PRO ASP LYS PHE
CCACCAAGTAACCCCTTGGCCAGATAGTTT
1900 1910 1920

LYS PRO ILE LEU GLY SER ASN ARG PRO
AGCCCATTTTAGGTTCAACAACAGACCC
1930 1940 1950

```

APPROVED	O.G.FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

SEQUENCE - 22524460

FIG.10J

```

      ILE CYS LEU ASP ALA TYR GLY TYR GLY HIS
      A T T G C C T T G A T G C C T T A T G G T T A T G G T C A T
      1960                                1970                                1980

ASP HIS PRO GLN ALA CYS ASN ALA LYS ASN
G A C C A T C C A C A G G C T T G T A A C G C C A A A A C
      1990                                2000                                2010

      SER THR TYR GLN ASN PHE ALA ILE LYS LYS
      A G C A C T T A T C A A A A C T T T G C C A T C A A A A A
      2020                                2030                                2040

GLY ILE GLU GLN TYR ASN GLN THR ASN THR
G G C A T A G A G C A A T A C A A C C A A T A C C
      2050                                2060                                2070

      ASP LYS ILE ASP TYR GLN ALA VAL ILE ASP
      G A T A A G A T T G A T T A T C A A G C C G T C A T T G A C
      2080                                2090                                2100

GLN TYR ASP LYS GLN ASN PRO ASN SER THR
C A A T A T G A T A A C A A A A C C C C A A C A G C A C C
      2110                                2120                                2130

      LEU LYS PRO PHE GLU LYS ILE LYS GLN SER
      C T A A A C C C C T T T G A G A A A A T C A A C A A A G T
      2140                                2150                                2160

```

FIG.10K

LEU GLY GLN GLY LYS TYR ASP GLU ILE ASP  
 TTGGGGCAAGAAATAACGACGAGATAGAC  
 2170 2180 2190  
 ARG LEU GLY PHE ASN ALA TYR LYS ASP LEU  
 AGACTGGGCTTTAATGCTTATAAGATTTA  
 2200 2210 2220  
 ARG ASN GLU TRP ALA GLY TRP THR ASN ASP  
 CGCAACGAAATGGCGGGTTGGACTAATGAC  
 2230 2240 2250  
 ASN SER GLN GLN ASN ALA ASN LYS GLY THR  
 AACAGCCACACAAACGCCAATAAAGGCCACG  
 2260 2270 2280  
 ASP ASN ILE TYR GLN PRO ASN ALA THR  
 GATAATATCTATCAGCCAAATCAGCAACT  
 2290 2300 2310  
 VAL VAL LYS ASP ASP LYS CYS LYS TYR SER  
 GTGGTCAAGAGATGACAAATGTATAATAGC  
 2320 2330 2340  
 GLU THR ASN SER TYR ALA ASP CYS SER THR  
 GAGACCAACAGCTATGCTGATTGCTCAACC  
 2350 2360 2370

60150-0254160  
 60150-0254160

APPROVED	O.G.FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

APPROVED	O.G.FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG.10L

WO 97/32980

36/90

09/142628

PCT/CA97/00163

THR ARG HIS ILE SER GLY ASP ASN TYR PHE  
A C T C G C C A C A T C A G C G G T G A T A T T A T T C  
2380 2390 2400

ILE ALA LEU LYS ASP ASN MET THR ILE ASN  
A T C G C T T A A A G A C A C A T G A C C A T C A A T  
2410 2420

LYS TYR VAL ASP LEU GLY LEU GLY ALA ARG  
A A A T A T G T T G A T T T G G G G C T G G G T G C T C G C  
2440 2450 2460

TYR ASP ARG ILE LYS HIS LYS SER ASP VAL  
T A T G A C A G A A T C A A C A C A A A T C T G A T G T G  
2470 2480 2490

PRO LEU VAL ASP ASN SER ALA SER ASN GLN  
C C T T G G T A G A C A C A C A G T G C C A G C A C C A G  
2500 2510 2520

LEU SER TRP ASN PHE GLY VAL VAL LYS  
C T G T C T T G G A A T T T T G G C G T G G T C G T C A G  
2530 2540 2550

PRO THR ASN TRP LEU ASP ILE ALA TYR ARG  
C C C A C C A A T T G G C T G G A C A T C G C T T A T A G A  
2560 2570 2580

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660190-82924160

## FIG.10M

```

SER  SER  GLN  GLY  PHE  ARG  MET  PRO  SER  PHE
AGCTCGCAAGGCTTTCGCATGCCAAGTTT
2590
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2600
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2610
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2620
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2630
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2640
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2650
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2660
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2670
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2680
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2690
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2700
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2710
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2720
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2730
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2740
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2750
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2760
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2770
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2780
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2790
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2800
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2810
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2820
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2830
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2840
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2850
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2860
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2870
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2880
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2890
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2900
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2910
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2920
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2930
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2940
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2950
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2960
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2970
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2980
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
2990
SER  GLU  MET  TYR  GLY  GLU  ARG  PHE  GLY  VAL
TCTGAATAGTATGGCGAACGCTTTGGCGTA
3000

```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660750-22524160

FIG.10N

TYR PHE LYS ASN ARG TYR THR ASP LEU ILE  
T A T T T A A A A T C G C T A T A C C G A T T T G A T T  
2800 2810 2820

VAL GLY LYS SER GLU GLU ILE ARG THR LEU  
G T T G G T A A A G T G A A G A G A T T A G A A C C C T A  
2830 2840 2850

THR GLN GLY ASP ASN ALA GLY LYS GLN ARG  
A C C C A A G G T G A T A A T G C A G G C A A A C A G C G T  
2860 2870 2880

GLY LYS GLY ASP LEU GLY PHE HIS ASN GLY  
G G T A A A G G T G A T T T G G C T T T C A T A A T G G G  
2890 2900 2910

GLN ASP ALA ASP LEU THR GLY ILE ASN ILE  
C A G A T G C T G A T T T G A C A G G C A T T A C A T T  
2920 2930 2940

LEU GLY ARG LEU ASP LEU ASN ALA VAL ASN  
C T T G G C A G A C T T G A C C T A A A C G C T G T C A A T  
2950 2960 2970

SER ARG LEU PRO TYR GLY LEU TYR SER THR  
A G T C G C C T T C C C T A T G G A T T A T A C T C A C A  
2980 2990 3000

APPROVED	03.FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

60F50-8292760

FIG.100

LEU ALA TYR ASN LYS VAL ASP VAL LYS GLY  
 CTGGCTTATAACAAGTTGATTAAAGGA  
 3010 3020 3030  
 LYS THR LEU ASN PRO THR LEU ALA GLY THR  
 AAAACCTTAAACCCAACTTGGCAGGACA  
 3040 3050 3060  
 ASN ILE LEU PHE ASP ALA ILE GLN PRO SER  
 AACATACCTGTTTGATGCCATTGAGCCATCT  
 3070 3080 3090  
 ARG TYR VAL VAL GLY LEU GLY TYR ASP ALA  
 CGTTATGTGGTGGGGCTTGGCTATGATGCC  
 3100 3110 3120  
 PRO SER GLN LYS TRP GLY ALA ASN ALA ILE  
 CCAAGCCCAAATAAGGAGCAACGCCATA  
 3130 3140 3150  
 PHE THR HIS SER ASP ALA LYS ASN PRO SER  
 TTACCCATTCTGATGCCCAAATAATCCAGC  
 3160 3170 3180  
 GLU LEU LEU ALA ASP LYS ASN LEU GLY ASN  
 GAGCTTTTGCGAGATAAGAACTTAGGTAA  
 3190 3200 3210

39/90

FIG.10P

500150" 3234160

APPROVED	O.G.FIG:	
BY	CLASS	SUBCLASS
DRAFTSMAN		

WO 97/32980

40/90

09/142628

PCT/CA97/00163

GLY ASN ILE GLN THR LYS GLN ALA THR LYS  
GGCAACATTCAACAAACAGCCACCAAA  
3220 3230 3240

ALA LYS SER THR PRO TRP GLN THR LEU ASP  
GCAAAATCCACCGCTGGCAACACTTGAT  
3250 3260 3270

LEU SER GLY TYR VAL ASN ILE LYS ASP ASN  
TTGTCAGGTATGTAAACATAAAGATAAT  
3280 3290 3300

PHE THR LEU ARG ALA GLY VAL TYR ASN VAL  
TTTACCCTTGCGTGCTGGCGTGTAATAATA  
3310 3320 3330

PHE ASN THR TYR TYR THR THR TRP GLU ALA  
TTTAATAACCTATTACACCACTTGGGAGGCT  
3340 3350 3360

LEU ARG GLN THR ALA GLU GLY ALA VAL ASN  
TTACGCCAACACAGCAGAGGGCGGTCAAT  
3370 3380 3390

GLN HIS THR GLY LEU SER GLN ASP LYS HIS  
CAGCATACAGGACTGAGCCAAAGATAAGCAT  
3400 3410 3420



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

600150 - 32980163

## FIG.10Q

TYR GLI ARG TYR ALA PRO GLY ARG ASN  
 TATGGTCGCTATGCCGCTCCCTGGACGCAAT 3430  
 3440  
 TYR GLN LEU ALA LEU GLU MET LYS PHE \*\*\*  
 TACCAATTGGCACTTGAAATGAAGTTTATAA 3450  
 S 3460  
 3470  
 3480  
 CCAGTGGCTTTGATGTGATCATGCCAATC 3490  
 3500  
 3510  
 CCAATCAACCAATGAATAAAGCCCCCATCT 3520  
 3530  
 3540  
 ACCATGAGGGCTTTATTTATCATCGCTGA 3550  
 3560  
 3570  
 GATGCTCTTAGCCGTCATCACTCAGATT 3580  
 3590  
 3600  
 GTCATTAAATTTATAGCGGATTAAATTTA 3610  
 3620  
 3630  
 GTAATCACGCTGCTCTTTGATGATTTAAG 3640  
 3650  
 3660

09/142628

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

660190-8234760

FIG.11A

Q8 tpbB Sequence.

```

CCTAGGGCTGACAGTAACAACACTTTATAC      30
      20
AGCACATCATTGATTTATTATCCCAAAATGCC      60
      40
ACACGCTATTATCTTTTGGGGCAGACTTT      90
      80
TATGATGAATAAAGTGCCACAAGACCCATCT      120
      100
GACAGCTATGAGCGTCGTGGCATACGCACA      150
      140
GCTTGGGGCAAGAAATGGGGCGGGCTCTT      180
      160
TCAAGCCGTGCCCAAATCAGCATCAACAAA      210
      200
CGCCATTACCAAGGAGCAAACTAACCCAGC      240
      220
GGTGGACAAATTCCGCCAGGATAAACAGATG      270
      260
CAAGCGTCTTTATTCGCTTTGGCACAGAGAC      300
      280

```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

500-500-500-500

FIG.11B

A T T C A C A A T G G G G C A T C A C G C C A C G G C T G 310 320 330  
 A C C A T C A G C A C A A C A T C A A T A A A G C A A T 340 350 360  
 G A C A T C A A G G C A A T T A T C A C A A A A T C A A 370 380 390  
 A T G T T T G T T G A G T T T A G T C G C A T T T T T G A 400 410 420  
 T G G G A T A A G C A T G C C C T A C T T T T G T T T T 430 440 450  
 G T A A A A A A T G T A C C A T C A T A G A C A A T A T C 460 470 480  
 A A G A A A A A T C A A G A A A A A G A T T A C A A A T 490 500 510  
 T T A A T G A T A A T T G T T A T T G T T T A T G T T A T T 520 530 540  
 A T T T A T C A A T G T A A A T T T G C C G T A T T T T G T 550 560 570  
 C C A T C A T A A A C G C A T T T A T C A A A T G C T C A A 580 590 600

09/142628

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

600150-2234160

## FIG.11C

```

A T A A T A C G C C A A T G C A C A T T G T C A A C A T      620
610
G C C A A A T A G G C A T T A C A G A C T T T T T A G      650
640
A T A A T A C C A T C A A C C C A T C A G A G A T T A T T      680
670
      MET LYS HIS ILE PRO LEU THR LEU C
      T T A T G A A C A C A C A T T C C T T T A C C A C T G T      710
      720

Y S   V A L   A L A   I L E   S E R   A L A   V A L   L E U   L E U   T H R
G T G T G C A A T C T C T G C C G T C T T A T T A C C G      740
730
      A L A   C Y S   G L Y   G L Y   S E R   S E R   G L Y   G L Y   P H E   A S N   P
      C T T G T G G T G G T A G C A G T G G T G G T T T C A A T C      770
      780

R O   P R O   A L A   S E R   T H R   P R O   I L E   P R O   A S N   A L A
C A C C T G C C T C T A C G C C C A T C C C A A A T G C A G      810
790
      G L Y   A S N   S E R   G L Y   A S N   A L A   G L Y   A S N   A L A   G L Y   A
      G T A A T T C A G G T A A T G C C T G G C A A T G C T G G C A      840
      830

```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

SEQUENCE

FIG.11D

SN ALA GLY GLY THR GLY GLY ALA ASN SER  
 A T G C T G G C G G T A C T G G C G G T G C A A A C T C T G  
 850 860 870  
 GLY ALA GLY ASN ALA GLY GLY THR GLY GLY A  
 G T G C A G G T A A T G C T G G C G G T A C T G G C G G T G  
 880 890 900  
 LA ASN SER GLY ALA GLY SER ALA SER THR  
 C A A C T C T G G T G C A G G C A G T G C C A G C A C A C  
 910 920 930  
 PRO GLU PRO LYS TYR LYS ASP VAL PRO THR A  
 C A G A C C A A A T A T A A A G A T G T G C C A A C C G  
 940 950 960  
 SP GLU ASN LYS LYS ALA GLU VAL SER GLY  
 A T G A A A A T A A A A A G C T G A A G T T T C A G G C A  
 970 980 990  
 ILE GLN GLU PRO ALA MET GLY TYR GLY VAL G  
 T T C A A G A A C C T G C C A T G G G T T A T G G C G T G G  
 1000 1010 1020  
 LU LEU LYS LEU ARG ASN TRP ILE PRO GLN  
 A A T T A A A G C T T C G T A A C T G G A T A C C A C A G  
 1030 1040 1050

45/90

FIG.11E

SEQUENCE

APPROVED	O.G.FIG.		
BY	CLASS	SUBCLASS	
DRAFTSMAN			

GLU GLN GLU GLU HIS ALA LYS ILE ASN THR A  
 AACAGGAAGAACATGCCAAATCAATACAA  
 1060 1070 1080

SN ASP VAL VAL LYS LEU GLU GLY ASP LEU  
 ATGATGTTGTAATACTTGAAAGGTGACTTGA  
 1090 1100 1110

LYS HIS ASN PRO PHE ASP ASN SER ILE TRP G  
 AGCATATAATCCATTTGACAACTCTATTGGC  
 1120 1130 1140

LN ASN ILE LYS ASN SER LYS GLU VAL GLN  
 AAACATCAAAATAGCAAGAGTACAA  
 1150 1160 1170

THR VAL TYR ASN GLN GLU LYS GLN ASN ILE G  
 CTGTTTACAACCAAGAGAGCAAAACATTG  
 1180 1190 1200

LU ASP GLN ILE LYS ARG GLU ASN LYS GLN  
 AGATCAATCAAAAGAGAAATAAACAA  
 1210 1220 1230

ARG PRO ASP LYS LYS LEU ASP ASP VAL ALA L  
 GCCCTGACAAATAAATTTGATGACGTGGCAC  
 1240 1250 1260

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG.11F

EU GLN ALA TYR ILE GLU LYS VAL LEU ASP  
 T A C A A G C T T A T T G A A A A G T T C T T G A T G  
 1270 1280 1290  
 ASP ARG LEU THR GLU LEU ALA LYS PRO ILE T  
 A C C G T C T A A C A G A A C T T G C T A A A C C C A T T T  
 1300 1310 1320  
 YR GLU LYS ASN ILE ASN TYR SER HIS ASP  
 A T G A A A A A A T A T T A T T C A C A T G A T A  
 1330 1340 1350  
 LYS GLN ASN LYS ALA ARG THR ARG ASP LEU L  
 A G C A G A A T A A A G C A C G C A C T C G T G A T T T G A  
 1360 1370 1380  
 YS TYR VAL ARG SER GLY TYR ILE TYR ARG  
 A G T A T G T G C G T T C T G G T T A T T T A T C G C T  
 1390 1400 1410  
 SER GLY TYR SER ASN ILE ILE PRO LYS LYS I  
 C A G G T T A T T C T A A T A T C A T T C C A A G A A A A  
 1420 1430 1440  
 LE ALA LYS THR GLY PHE ASP GLY ALA LEU  
 T A G C T A A A C T G G T T T T G A T G G T G C T T T A T  
 1450 1460 1470

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

SEQUENCE

FIG.11G

PHE TYR GLN GLY THR GLN THR ALA LYS GLN L  
 T T A T C A A G G T A C A C A A A C T G C T A A A C A A T  
 1480 1490 1500

EU PRO VAL SER GLN VAL LYS TYR LYS GLY  
 T G C C T G T A T C T C A A G T T A A G T A T A A A G G C A  
 1510 1520 1530

THR TRP ASP PHE MET THR ASP ALA LYS LYS G  
 C T T G G G A T T T A T G A C C G A T G C C A A A A A A G  
 1540 1550 1560

LY GLN SER PHE SER SER PHE GLY THR SER  
 G A C A A T C A T T A G C A G T T T G G T A C A T C G C  
 1570 1580 1590

GLN ARG LEU ALA GLY ASP ARG TYR SER ALA M  
 A A C G T C T T G C T G G T G A T C G T T A T A G T G C A A  
 1600 1610 1620

ET SER TYR HIS GLU TYR PRO SER LEU LEU  
 T G T C T T A C C A T G A A T A C C C A T C T T T A T T A A  
 1630 1640 1650

THR ASP GLU LYS ASN LYS PRO ASP ASN TYR A  
 C T G A T G A G A A A A C A A C C A G A T A T A T A  
 1660 1670 1680



**FIG. 11H**

[illegible]

TYR ASP ILE ILE ASP ALA ASN ILE TYR GLY ASN  
 ATGACA TCGATGCCAATACTACGGCAACC  
 1810 1820 1830  
 ARG PHE ARG GLY SER ALA THR ALA SER ASP T  
 GCTTCCTGGCAGTGCCACCGCAAGCGATA  
 1840 1850 1860

THR	THR	GLU	ALA	SER	LYS	SER	LYS	HIS	PRO
C	A	C	A	G	A	G	C	A	A
C	A	C	A	G	C	A	A	A	G
C	C	T							
			1870			1880			1890

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
GRAFTSKAH		

LEU ASP ALA TYR ALA LEU GLY THR PHE  
TCTTAGATGCCCTATGCACCTTGGGACATTTA  
2050 2060 2070  
ASN LYS PRO GLY THR THR ASN PRO ALA PHE T  
ATAACCTGGGTACGACCAATCCGCCCTTA  
2080 2090 2100

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

RECEIVED

FIG.11J

```

HR  ALA  ASN  SER  LYS  LYS  GLU  LEU  ASP  ASN
CCGCTAACAGCAAAAGAACTGGATAACT
2110
2120
2130
PHE  GLY  ASN  ALA  LYS  LYS  LEU  VAL  LEU  GLY  S
TTGGCAATGCCCAAAGTTGGTCTTGGGTT
2140
2150
2160

ER  THR  VAL  ILE  ASP  LEU  VAL  PRO  THR  GLY
CTACCGTCATTGATTGTTGCCCTACCGGTG
2170
2180
2190
ALA  THR  LYS  ASP  VAL  ASN  GLU  PHE  LYS  GLU  L
CCACCAAGATGTCAATGAATTCAAGAA
2200
2210
2220

YS  PRO  LYS  SER  ALA  THR  ASN  LYS  ALA  GLY
AGCCAAAGTCTGCCCAACAACAAGCGGCG
2230
2240
2250
GLU  THR  LEU  MET  VAL  ASN  ASP  GLU  VAL  ILE  V
AGACTTTGATGGTGAAATGATGAGTTATCG
2260
2270
2280

AL  LYS  THR  TYR  GLY  TYR  GLY  ARG  ASN  PHE
TCAAAACCTATTGGCTATTGGCAGAACTTTG
2290
2300
2310

```

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660150" 82541160

## FIG.11K

GLU TYR LEU LYS PHE GLY GLU LEU SER ILE G  
 AATACCTAAATTTGGTGAGCTTAGTATCG 2320 2340

LY GLY SER HIS SER VAL PHE LEU GLN GLY  
 GTGGTAGCCATAGCGTCTTTTACAAAGCGG 2350 2370

GLU ARG THR ALA GLU LYS ALA VAL PRO THR G  
 ACGCACCGCTGAGAAAGCCGTACCAACCG 2380 2400

LU GLY THR ALA LYS TYR LEU GLY ASN TRP  
 AGGCACAGCCAAATATCTGGGGAAC TGGG 2410 2430

VAL GLY TYR ILE THR GLY LYS ASP THR GLY T  
 TAGGATACATCACAGGAAGGACACAGGAA 2440 2460

HR SER THR GLY LYS SER PHE ASN GLU ALA  
 CGAGCACAGGAAAGAGCTTTAATGAGGCC 2470 2490

GLN ASP ILE ALA ASP PHE ASP ILE ASP PHE G  
 AAGATATTGCTGATTTTGACATTGACTTTG 2500 2520

09/142628

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 11L

FIG.11L

LU ARG LYS SER VAL LYS GLY LYS LEU THR  
 A G A G A A A T C A G T T A A A G G C A A A C T G A C C A 2540  
 2530  
 THR GLN GLY ARG GLN ASP PRO VAL PHE ASN I  
 C C C A A G G C C G C C A A G A C C C T G T A T T T A A C A 2580  
 2560  
 LE THR GLY GLN ILE ALA GLY ASN GLY TRP  
 T C A C A G G T C A A A T C G C A G G T A A T G G C T G G A 2600  
 2590  
 THR GLY THR ALA SER THR ALA LYS ALA ASN V  
 C A G G C A C A G C C A G C C C C C A A A G C G A A C G 2640  
 2620  
 AL GLY GLY TYR LYS ILE ASP SER SER SER  
 T A G G G G G C T A C A A G A T A G A T T C T A G C A G T A 2660  
 2650  
 THR GLY LYS SER ILE VAL ILE GLU ASN ALA L  
 C A G G C A A A T C C A T C G T C A T C G A A A A T G C C A 2700  
 2680  
 YS VAL THR GLY GLY PHE TYR TYR GLY PRO ASN  
 A G G T T A C A G G T G G C T T T T A T G G T C C A A A T G 2730  
 2710

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

600F50-3354160

# FIG.11M

ALA ASN GLU MET GLY GLY PHE THR HIS A  
CAAACGAGATGGGCGGGTCAATTACACACG 2750 2760

SP THR ASP ASP SER LYS ALA SER VAL VAL  
ATACCGATGACAGTAAAGCCCTCTGTGGTCT 2770 2780 2790

PHE GLY THR LYS ARG GLN GLU VAL LYS \*  
TTGGCACAAAGACACAGAGAGTTAGT 2800 2810 2820

\*\*

AGTAATTAAACACAATGCTTGGTTCGGCT 2830 2840 2850

GATGGGATTGACGCTTAATCAACATGAAT 2860 2870 2880

GATTAGATGATAAACCCATGCCAA 2890 2900 2910

TGATTGATAGCAACGATGGCAGATGAG 2920 2930 2940

TTTCA TTATCTGCCATTATTGCTTAA 2950 2960 2970

TTATTGCTTGTCATTGGTGGTGTATCAC 2980 2990 3000

FIG.11N

A T T A A T C A T T A A A T T A A C A T A A T A A T G A 3010  
 3020  
 T T A A A T G A T A T T T A A T G A A A G T C A G G T T A 3040  
 3050 3060  
  
 T T T T G G T C A T G G T T T T C A T G A T T A T T A A 3070  
 3080 3090  
 C T T A T A A T G C G T T A T G G T T A G C A A A A G C T 3100  
 3110 3120  
  
 A A G T C T G T C A A T G A A G C T A T G G T G A G T G A T 3130  
 3140 3150  
 T G T G C A A A A G A T G G T C A A A A A A T C G G T A T 3160  
 3170 3180  
  
 G G T G C T G T C A G G C G T G G T G A T G G T T C T G T T 3190  
 3200 3210  
 A A T G A T A A T A A C A A C G C C A A G C C A T G C T A C 3220  
 3230 3240  
  
 T G C C A A G T T G T T G C C G A C C T C T C A G A A A A 3250  
 3260 3270  
 T C C A A C C A A A A C T A T G G T A G A T A G C T T T G G 3280  
 3290 3300

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

60150" Section

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

660150-SECRET

# FIG.11.0

TCGTGAAACGCCACGAGGGGCA GTTCAGGG  
3310 3320 3330

GCTATTGCCGTGCAATTGCAGCAGAA GACTA  
3340 3350 3360

TGAGCTGGCTGCCA ACTATT TGGACGGCCG  
3370 3380 3390

TTATTGGCAAA AACCCCAAACGCCCAATCG  
3400 3410 3420

TGAGATTGTTGAGCA  
3430



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

660750" 82924760

FIG.12A

Tbp1 alignment

	10	20	30	40	50	60	
MNQSKQNNKSKKQVLKLSALSLGLINI--TQVALANTTADKAEF-TDKTNLWVLDFTVVT							
.....							
.Q.QHLFR-----NILC-----MT.PVY-----NVQAEQAEKQ..TIQ.K							
.Q.QHLFR-----NILC-----MT.PAY-----NVQAEQAEKQ..TIQ.K							
.Q.QHLFR-----NILC-----MT.PAY-----NVQAEQAEKQ..TIQ.K							
.TKKPYFR-----LSIISC.LI.CYVKAEE.SIKDIKE.ISS.VD.QS.E-DSE.ETIS..							
							70
							80
							90
							100
AKKNA-RKANEVTGLGKWKTAETINKEQVLNIRDLTRYDP							4223
.....							Q8
...QKT.RD.....L..SSD.LS.....							B16B6
...QKT.RD.....L...D.LS....D.....							M982
...QKT.RD.....L...D.LS....D.....							FA19
.E.IRD..D.....II..S.S.SR.....							Eagan

	110	120	130	140	150	160
GLIAVVEQFGASSGYSIRGMDKNR/AVLVLDGINQAQHYALQCPVAGKNYA-ACGAINETIYEN						
.....						
.....SLT...VS.I.S.TA.AALG.TRT.GSS.....						
.....SLT...LA.I.S.TA.AALG.TRT.GSS.....						
.....SLT...LA.I.S.TA.AALG.TRT.GSS.....						
..S.....R...L...LP.T.S.W.S.LVATSGYSGT.....						

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

FIG. 12B

FIG.12B

WO 97/32980

58/90

09/142628

PCT/CA97/00163

170 180 190 200 4223  
 VRSVEISKANSSEYSGSALSGSVAFVTKTADDIIKDG  
 .....  
 .KA.....S.....N...A.....Q....A...GE.  
 .KA.....S.V.Q.....A.....Q.....V.GE.  
 .KA.....S.V.Q.....A.....Q.....V.GE.  
 .KA.....GS.....N...A...T.QS.S.A..LEGD  
 Q8  
 B16B6  
 M982  
 FA19  
 Eagan

210 220 230 240 250 260  
 KDWGVQTKTAYASKNNAMNSVAAAGKAGSFSGLIIYTDPRGQYKAHDDAYQGSQSFDRAVA  
 .....  
 .Q..I.S....SG.DH.LTQ.L.L..RS.GAEA.L...K...R.IH..K..GK.V...N.L.L  
 RQ..I.S....SG..RGLTQ.I.L..RI.GAEA.L.H.G..AG.IR..E..GR.V...N.L.P  
 RQ..I.S....SG..RGLTQ.I.L..RI.GAEA.L.H.G.HAG.IR..EA.GR.V...N.LAP  
 .S..I...N..S...KGFTH.L.V...Q.G.E..A...Q.NSI.TQV.K..LK.V..Y..LI.

270 280 290 300 4223  
 TTD-----PNNRTFLIANECANFENYEACAAGGQTKLOAKPTN  
 .....PK.....  
 DE.KKEGGSQY.Y.IVEE..H...-A..KNKL--ED.SVKD  
 VE.-----SSEYAY.IVED..EGK...T.KSKP--KDWGKD  
 VE.-----GSKYAY.IVEE..K..GH.K.K.NP--KDWGED  
 ...-----KSSGY.V.QG..P..DDK-...-----PP.TLST  
 Q8  
 B16B6  
 M982  
 FA19  
 Eagan

APPROVED	O.G. FIG.	
BY	CLAYS	SUBCLASS
CRAFTSMAN		

660150" 82941160

FIG. 12C

310	320	330	340	350	360	
VRDKVNVKDYTGPNRLIPNPLTQDSKSLILRPGYLNDK-HVVGVEITKQNYAMQDKTVPA						
.....						
E.KT.STQ.....S..LA...EYG.Q.W.F...WH.DNR-...A.L.R.Q.TFDIR.M....						
E.QT.STR.....FLAD..SYE.R.W.F...FRFENKR..I..IL.H.Q.TFDIR.M....						
K.QT.STR.....FLAD..SYE.R.W.F...FRFENKR..I..IL.R.Q.TFDIR.M....						
QSET.S.S...A..IK...MKYE.Q.WF..G..HFSEQ-.I..IF.F.Q.KFDIR.M.F...						
	370	380	390	400		
	YLTVHDIKSRLSNHAQA--NGYYQGNLGERIRDITIGPD				4223	
	.....G..--.....A..AN				Q8	
	.F.SE.YVPGS.KGL-----K.S.D.KA..LFVQGECS				B16B6	
	F..KAVFDANSKQAGSLPG-.K.A..HKYGLFTINGENG				M982	
	F..KAVFDANQKQAGSLPG-.K.A..HKYGLFTSGENN				FA19	
	..SPTERDDSSRSFYPMQDH.A..HIE-----				Eagan	
	410	420	430	440	450	460
-----SGYGINYAHGVFYDEKHQKDELGLEVVYDSKGENKWFDDVRVSYDKQDITLRSQLTNTHC						
-----						
TLQGI...---T.....R.T.N.Y.V...HNADKDT.A.YA.L...R.G.D.DNR.QQ...						
-----ALV.AE.GT.....T.T.S.Y.....TNADKDT.A.YA.L...R.G.G.DNHQQ...						
-----APV.AE.GT.....T.T.S.Y.....TNADKDT.A.YA.L...R.G.G.DNHQQ...						
-----D.R.VK..S.LYF..H.R.Q.V.I..I.EN.NKAGII.KAVL.ANQ.N.I.D.YMRH...						

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

FIG.12D

WO 97/32980

60/90

09/142628

PCT/CA97/00163

470 480 490 500  
STYPHIDKNCPTDVKPFSVKEVDNNAYKEQHNLKAVFN  
.....R.G...Y.FYKS.RMI.E.SR..FQ...K  
.HDGS-...R.G...Y.FYKS.RMI.E.SR..FQ...K  
.ADGS-...Y.R.SAD...YYKS.RVI.G.S.R.LQ.A.K  
.ADGS-...Y.R.SAD...YYKS.RVI.G.S.R.LQ.A.K  
.L..NPS...R.TLD..Y.YYRS.R.V...K..MLQINLE

4223  
Q8  
B16B6  
M982  
FA19  
Eagan

510 520 530 540 550 560  
KKMALGSTHHHINLQVGYDKFNSSLREDYRLATHQSYQKLDYTPPSNPLPKF-KPILGSNN  
.....N.....  
.AFDTAKIR.NLSINL...R.K.Q..HS..Y.QNAVQAYD.I-...KP.F.NGS-.....D  
.SFDTAJUR.NKSVNK.F.R.S.B.RHQ..YYQHANRAYSSK-...KTAN.NGD-.....S  
.SFDTAKIR.NLSVNL...T.G.N.RHQ..YYQSANRAYS.K-...Q.NGKTS-...PN.REK  
...IQQNMLT.Q.VFNL.F.D.T.A.QHK..-..TRRVIATA-.SI.RK-...GETG..RN.LQS

570 580 590 600  
KPICLDAYGYGHDHPQACNAKNSTYQNFALKKGIEQYN  
R.....  
N.YRVSIGK-----  
..YWVSIG-----  
N.YWVSIGR-----  
Q.YLYPKPEP-----

4223  
Q8  
B16B6  
M982  
FA19  
Eagan

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

[illegible]

**FIG. 12E**

610	620	630	640	650	660
OKTNTDKIDYQALIDQYDKQNPENSTLKPFEKIKQSLGOEKYNKIDELGFKAYKIDLRNEWAGMT					
-.....V.....DE..R..N.....					

670	680	690	700	
NDNSQVANKGRDNIYQPNQ	-TVVKDDKCKYSETNS-Y			4223
.....	.....			Q8
-----	T..NTSPI.RFCN-.T-. .			B16B6
-----	GN..TGQI.LFCN-.T-. .			M982
-----	GN..TRQI.LFCN-.T-. .			FA19
-----	YFAGQDH-.N.QGSS.N.			Eagan

710	720	730	740	750	760
ADCSTTRH	ISGDN	YFALKDN	MTINKYVD	LGARYD	RIKHKSDV
PLVDNSA	SNQLSW	FEGW			
T. - P. N. G. NG. YA. VQ. .	VRIGRWA. V. A. I. .	YRSTH. EDKS. STGTHRN. . .	A. . .		
T. - P. S. N. KS. YA. VR. .	VRIGRWA. V. A. L. .	YRSTH. DGS. STGTHRT. . .	A. I. .		
T. - P. S. N. KS. YA. VR. .	VRIGRWA. V. A. L. .	YRSTH. DGS. STGTHRT. . .	A. I. .		
R. - KV. L. K. K. YF. ARN. .	ALG. . . . .	I. . . . .	VSRT. ANESTISVGEKFN. . .	T. I. .	

[illegible]

FIG. 12F

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

770	780	790	800	
VVKPTNMLDIAYRSSQGRMPSEMYGERRFGVTICKG				4223
.....				Q8
L..FT.M.LT..A.T..L..A...W.A.ESLCTL				B16B6
L..AD...LT..T.T..L..A...W.S.OSKAV				M982
L..AD...LT..T.T..L..A...W.S.DK.KAV				FA19
I..E...LS..L.T..N.....W.Y.GKNDIV				Eagan

810	820	830	840	850	860
TOHGCKGLYYICQQT	VHQT	KLKPEKSFNQ	EIGATLHNH	LGSLVSYFKNRY	TDLIVKSEEIFR
.....	.....	.....	.....	.....	.....
-----	D.....	R.A.IVFKGDF	N.A...N.A.R...	AFGY-.T.	
-----	ID.....	K.A.IVFKGDF	N.A.W.N.A.R...	RGY.AQI	
-----	ID.....	K.A.IVFKGDF	N.A.W.N.A.R...	RGY.AQI	
-----	YVG.F...T.R...	F.LA.KGDF	NI.I.H.S.A.RN.	AF.A-.LS	

870	880	890	900	
TLITQDNAGKQKGKDLGFHNGQDADLTGTINILGRLD				4223
.....N.....K..				Q8
-----QN.QTSAS..P.YR.A.N.RIA.....KI..				B16B6
KK-----N..EEA...PAYL.A.S.RI.....KI..				M982
KK-----D..EQV..NPAYL.A.S.RI.....KI..				FA19
KK-----NGT...NY.Y..A.N.K.V.V..TAQ...				Eagan

FIG.12G

APPROVED	O.G.FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

FIG. 12G

910 920 930 940 950 960  
LNAVNSRLPYGLYSTLAVNKVDVKGTINPTLAG-TNILFDAIQPSRYVVGGLGYDAPSQKMG  
.....  
WHG.WGG.D.....RIK.DADIRADRTFV.SY...V.....L.....H.DGI.I  
WNG.WDK.E.W...F...R.H.RDIKKRADRTDIQSH.....Q.EG...V  
WNG.WDK.E.W...F...R.H.RDIKKRADRTDIQSH.....S...Q.EG...V  
F.GLMK.I...W.A.F...Q.K..DQKI.AG..SVSSY.....II.....H.NT..I

970 980 990 1000  
NAIFTHSDAKNPSELLADKNLGNENIQ-TKQATKAKSTP

4223  
Q8  
B16B6  
M982  
FA19  
Eagan

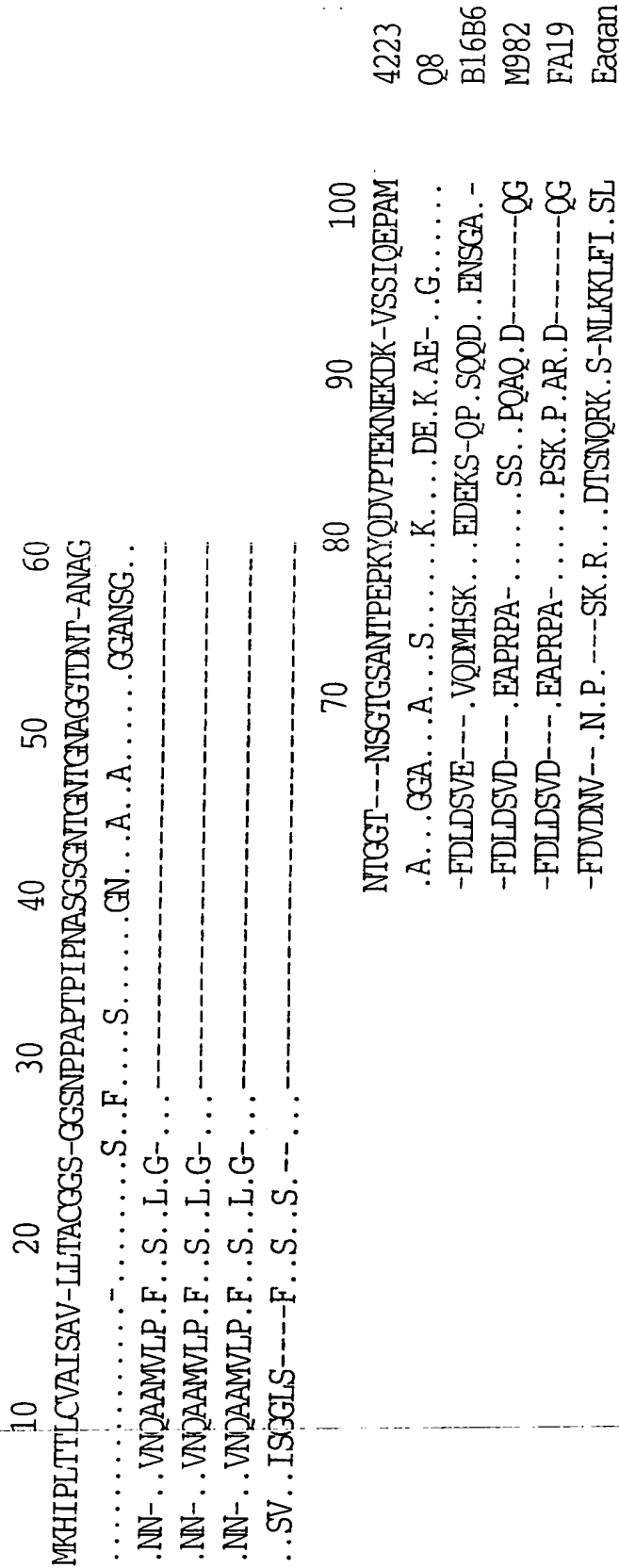
1010 1020 1030 1040 1050 1060 1070  
WQTLDLGSYVNIKNFTLRAGVYNVFNFTYTTWEALRQTAEGAVNQHTGLSQDKHYGRYAAPGRNYQLAEMKF\* 4223  
.....  
YVT.V...Y...KHL.....LL.YR.V...NV...G.....---KNVGV.N.....TFS.....\*  
YIV.V...YT...KH.....LL.YR.V...NV...G.....---KNVGV.N.....TFS.....\*  
YIV.V...YTV.KH.....LL.HR.V...NV...A.....---KNVGV.N.....TFS.....\*  
HI.V...YMANK.IM.L.I..L..YR.V...V...Q.....---QNVGS.T...S...T.T.....\*  
.....Eagan

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

600F50" sheet 60

FIG.13A

Tbp2 comparison



110	120	130	140	150
GYGMALSKINLHNRQDTPLD-EKNIITL--DGKKQVAEG-KKSPLPFS-LDV-ENKLLDGZIA				
...VE.-.LRNWIP.EQEEH-A.IN-.N--.VV.LEGDL-.HN.FDN.IWQNIK.SKEVQIVY				
...F.V-.LPRR.AHFN.KYK..HKP.GSM.W-----LQGEPSFS.RDE.E----				
...F.M-RUKRR.WYP--GAE.SEVK.NES.WEATGLPTKP.E-...KRQKS.I.KVET..D-S				
...F.M-RFKRR.WHPSANPK.DEVK.KND.WEATGLPTEP.K-..LKQQS.ISEVEIN.N-S				
.G.K.VAQ..RGNKEPSFLN.DDY.-----SY..S.STI.KDVK.NNK-				



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

FIG.13B

160 170 180 190 200 4223  
KMNADKNAIGDRIKKNKEISDEELAKQIKEAVRKSHEFOQV-  
NQEKNIEDQIK.EN.QRPDKLDDV.L.AYIEKVLDDRLTELA  
-----K.R.SS.LI-.SKWEDQSR.VGYTN.T---  
DIYSSPYLTPSNHONG-----AGNGVN.P.NOATGHEN.---  
..YTSPYLSQDADS-----HANG.N.P.NE.TDYKK.-----  
--G.--L..S-.-----PSTINPP.K-----HG.---

210 220 230 240 250 260  
LSSLENKIFHSNDGTTKATTRDLKYVDYGY-YLANDGNVLTVTDKLWNLGPPVGVFYNGTTT  
KPIY.KN.NY.H.KQN..R.....RS..I.RSGYS.---IIPK.IAKT.FD.AL..Q..Q.  
-----RS..V..-KN.IDIKNNIV.F---D.YLY.K.KEP  
-----YS.WF.KH.ASEKDFSN.KI.S---DD.YI..H.EK  
-----YS.WF.KH.KSEVKNENGLVSAKR-.D.YI..H.DK  
-----YS.LY.TPSWSLINDS-.N-.FY-.YY.YA..Y.NK.

270 280 290 300 4223  
AKELPTQDAVKYKGHWDFMTDVANRRNRFSEVKENS--QA  
..Q..VSQ-.....T.....-KKGQS..SFGT-.QRL.  
S....-SEKIT...T..YV.AME-KQ...-GLG-.A..G  
PSRQ..ASGK.I...V.H.V..TKKGQD.R.IIQP.KK.G  
PSRQ..ASE..T...V.H.V..TKQGQK.NDIL.T.KG.G  
..TN..VNGVA....T...I.ATK.-GK.YPLLSNG.H.--

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

660450" 62541160

FIG.13C

310 320 330 340 350 360  
 GWYYGASSKD-EYNRLITKEDSAPDGHSGEYGHSEFTVNFKEKKLTGKLSN---LQDRHKCN  
 .DR.S.M.YH-.PS..D.KNK..NYN.....D.SK.S.K.E.S..---I..G...S  
 DK-S..L.AL-.EGV.RNQAE-ASS..TD-F.MT...E.D.SD.TIK.T.YR.NRIT.NNSENK  
 DR.S.F.GDGS.EYSNKN-.STLK.D.E.-..FT.NLE.D.GN.....IR.NAS.NNNINND  
 DK.S.F.GDEG.TTSNR.-DSNLN.K.E.-..FT.N.K.D.NM.....IR.NKVINTAASDG  
 ---RR-.AIP.DID.EN-DSKNG.-I.-----LI....SADGGT.....Q.-.YTKRKTNNQPYE  
 370 380 390 400

VTKTERYDIDANIHCNFRGSAATSNK--NDTSK-HPFTSDAN 4223  
 .N..K.....Y.....DTTEASK..-.....K Q8  
 QI..T..T.Q.TL.....K.K.L.AD.--GA.NGS...I..SD B16B6  
 KHT.QY.SL..Q.T...N.T...TD.K-ENET.L...V..SS M982  
 Y..Y.SL..TLR....S.K.I.TD.PNIGGT.L...VF.SS FA19  
 KK.L--.....D.YS.....TVKPTE.---SEE-.....EGT Eagan

410 420 430 440  
 NRLEGGFYGPKEELACKFLTNKLVFGAKRESK-----AEEKTE-----  
 .S.....NA.....E-----K....-----  
 S-.....S...VAA.....QKD.KDGENA.GPA.....  
 S-S...F..Q....GFR..SD.Q.VAV.GS...TKD.LENGAA.SGS.G-AAASGGAAGTSSE  
 S-S...F..Q....GFR..SD.G.VAV.GS...TKDST-----NGNAP-AASSGPGAATMPS  
 ---.....NA...G....AT..RV....S..ETEETKEALS.K.TLIDGKLITFTKKIDA

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 13D

FIG.13D

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67/90

PCT/CA97/00163

97/142628

450 460 470 480  
 ----AIIIDAYALGTFNFSNAT--TFPTPTEKQIDNFGNAKLV 4223  
 ----KPGT.NPA..ANSK.E..... Q8  
 ----TVI...RIT-----GEEFKKE.I.S.DV...L B16B6  
 NSKLTIV...VE.T-----LNDKKI.N....S..AQ.. M982  
 ETRLTIV...VE.T-----PDGKEI.N....S..TR.. FA19  
 KINATTSTA.NTTIDTANTI.D--EKN.KTEDISS..E.DY.L Eagan

490 510 520  
 LGSTVIDLVP-----TDATK--NEFTKDK---PESATNEAGEITMDEVSV-----  
 .....G...DV...E...K...K.....I.-----  
 VDGVELS.L.--SE-GNKAA-----FQHEI.  
 VDGIM.P.L.KDSESGNTQADKGNKG--T...RKFHT...DKKD.QAGTQINGAQIASNIA  
 VDGIM.P.L.--TESGNGQADKGNKG--TD..YEITYT...DKKDIKAQIGAGCMQTASGIA  
 IDKYP.P.L.-----DKNTN-----FI.SK-----

530 540  
 ----KTYGKN-----FEYLFKGELSIGGSH 4223  
 ----YGRN----- Q8  
 --QNGVKAT-----VCCSNLD.MS..K..KENKD B16B6  
 GDINGK--T...EVE-VCCSNIN...Y.M.TRKN.K M982  
 GVNGGQVGT...KVQ-VCCSNIN...Y.L..RENNN FA19  
 --HHTVGN-.R.KVEAVCCSNISDVKS.MYVEDPLKE Eagan

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/142628

WO 97/32980

68/90

PCT/CA97/00163

FIG.13E

550 560 570  
 -----SVFLQCERTATIGEKAVPTIGTAKYLG  
 -----E.....  
 -----DM...V..PVSDVA.-R.EAN...R.  
 SAMQAG-----NSSQADAKTEQVEQ.M.....-D..EI..DQNV.R.  
 SVMQAVK-----NSSQADAKTKQIEQ.M.....-D.NKI.QEQGIV...  
 KETETETETEKDEKEKDEKQTAATINTYYQ--..L.H..---PKDDI.K.S...H.

580 590 600 610  
 NMWGYIT-GKDIGIGTGSFYDAQDVADFTIDFGNKSVSCK  
 .....S.....NE...I...D...ER...K..  
 T.Y...AN.-TSWS.EA-.NOEGENR.E.DV..ST.KI..T  
 S.Y.H.AN.-TSWS.NA-.DKEGENR.E..VN.AD.KIT..  
 F.Y.R.AN.-TSWS.KA-.NATDGENR.K..VN.DR.EIT.T  
 S.Y....D..TSYSPS.DKKR.KNA..E.NV..AE.KLT.E

4223  
 Q8  
 B16B6  
 M982  
 FA19  
 Eagan

620 630 640 650 660 670  
 LITKGRQDPVFSITGQIAG--NGMIGTASITTKADAGYKIDSSSTGKSIA--IKDANVTGCFYG  
 .T.Q.....N.....A.NV.....V--.EN.K.....  
 .TA.D.TS.A.T..AM.KD--..FS.V.K.---GEN.FAL.PQN..N.HYTH.-E.T.S.....  
 .TAEN..AQT.T.E.M.Q.--..FE...K.---AES.FDL.QKN.TRIPKAY.T.K.K.....  
 .TAEN.SEAT.T.DAM.E.--..FK...K.---GND.FAP.QNNSTVTHKVH.AN.E.Q.....  
 .KRHDTCN.....EAFNNS.AF....TA.-----NFV..GKNSQNKVTPNITTK.N.A....

650150-8294160

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
BRAFTSHAH		

WO 97/32980

69/90

09/142628  
PCT/CA97/00163

FIG.13F

680  
PNANEMGGSFT-----NADDSKASV  
.....HDT.....  
K..I.....SFFGNAPEGKOE-----  
.K.E.L..W.AYFGDKQTEKATATSSDG---.SAS.-.T.  
...E.L..W.AYFGNEQTKNAIVESGNG---.SAS.-.T.  
.K.S.L..Y..YNGNSTATNSESSTVSSSS.SKNAP.A.

4223  
Q8  
B16B6  
M982  
FA19  
Eagan

700  
VFGTKRQOEK-K\*  
.....E.-.\*  
...A....L.Q-\*  
...A....P.Q-\*  
...A....K.L.-.\*  
...ARQ.V.TT.\*

4223  
Q8  
B16B6  
M982  
FA19  
Eagan

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
BRAFTSHAH		

660150-6294160

WO 97/32980

70/90

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PCT/CA97/00163

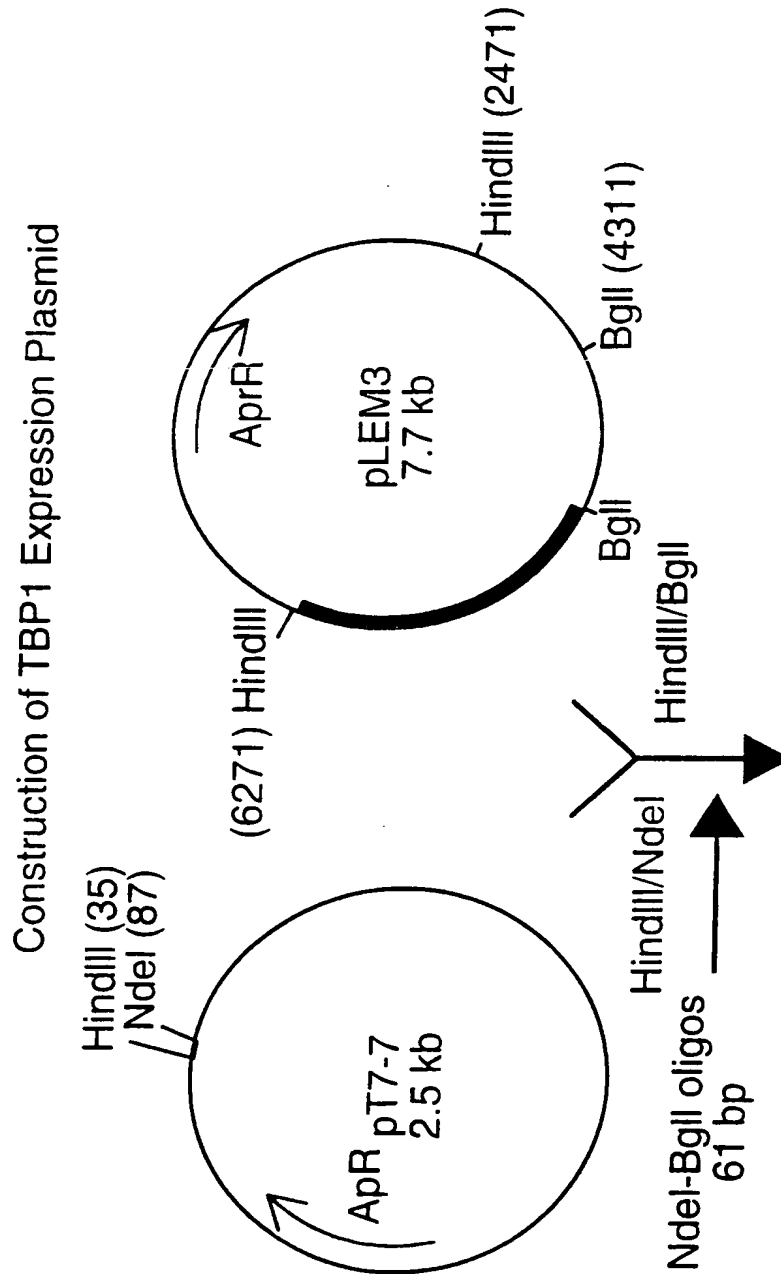


FIG.14A

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

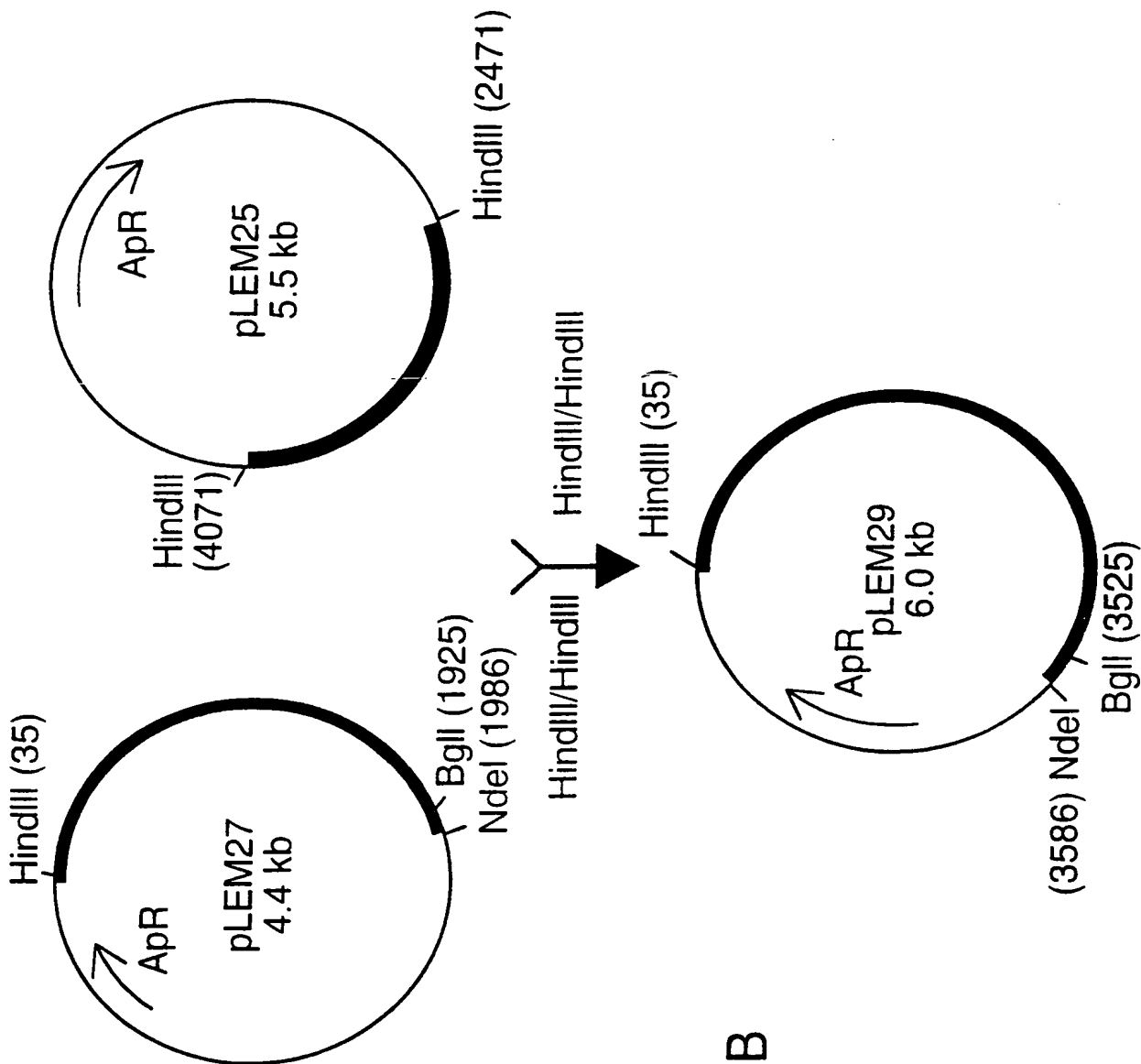
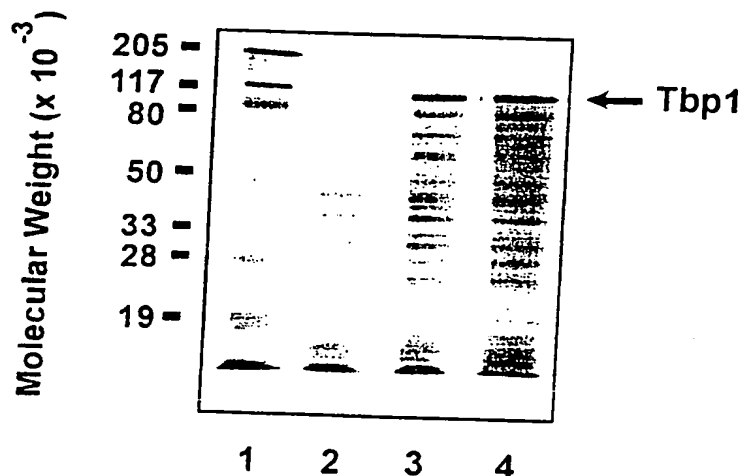


FIG.14B

# Expression of rTbp1 in *E. coli*

APPROVED BY BRAFTSHAN	O.G. FIG.	
	CLASS	SUBCLASS



1. Prestained molecular weight markers
2. pLEM29B-1 lysate, non-induced
3. pLEM29B-1 lysate, 1 hr post-induction
4. pLEM29B-1 lysate, 3 hr post-induction

Fig.15



Purification of Tbp1 from *E. Cole*

O.G. FIG.	CLASS	
	SUBCLASS	
APPROVED	BY	DRAFTSMAN

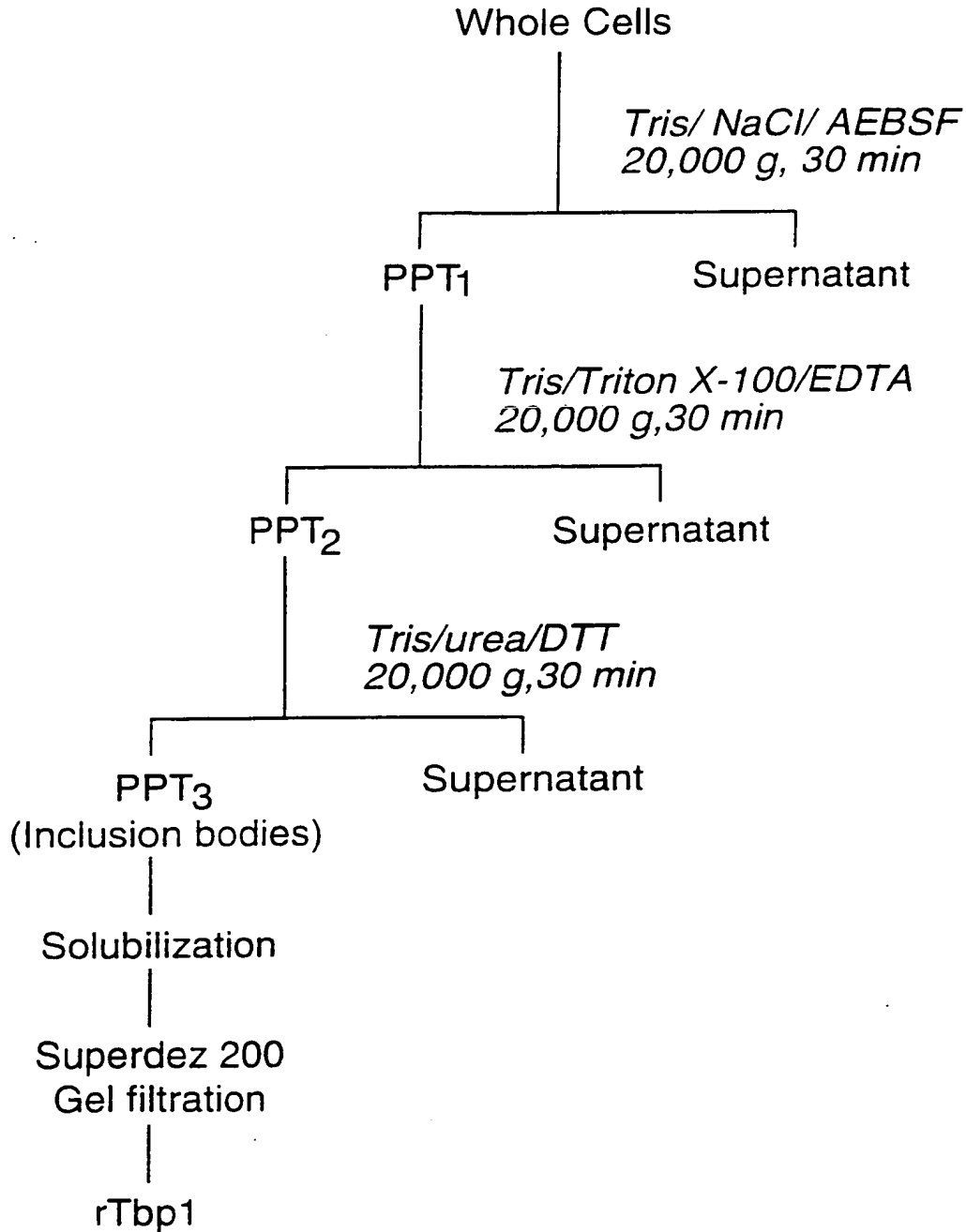
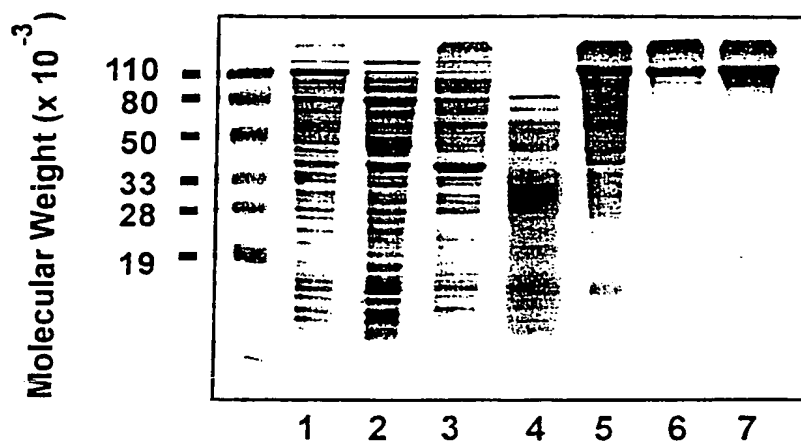


FIG.16

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

# Purification of rTbp1 from *E. coli*



1. *E. coli* Whole cells
2. Soluble proteins after 50 mM Tris/ NaCl extraction
3. Soluble proteins after Tris/ Triton X-100/ EDTA extraction
4. Soluble proteins after Tris/ urea/ DTT extraction
5. Left-over pellet (rTbp1 inclusion bodies)
- 6.7. Purified rTbp1

Fig.17

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

660150-2254160

# CONSTRUCTION OF TBP2 EXPRESSION PLASMID

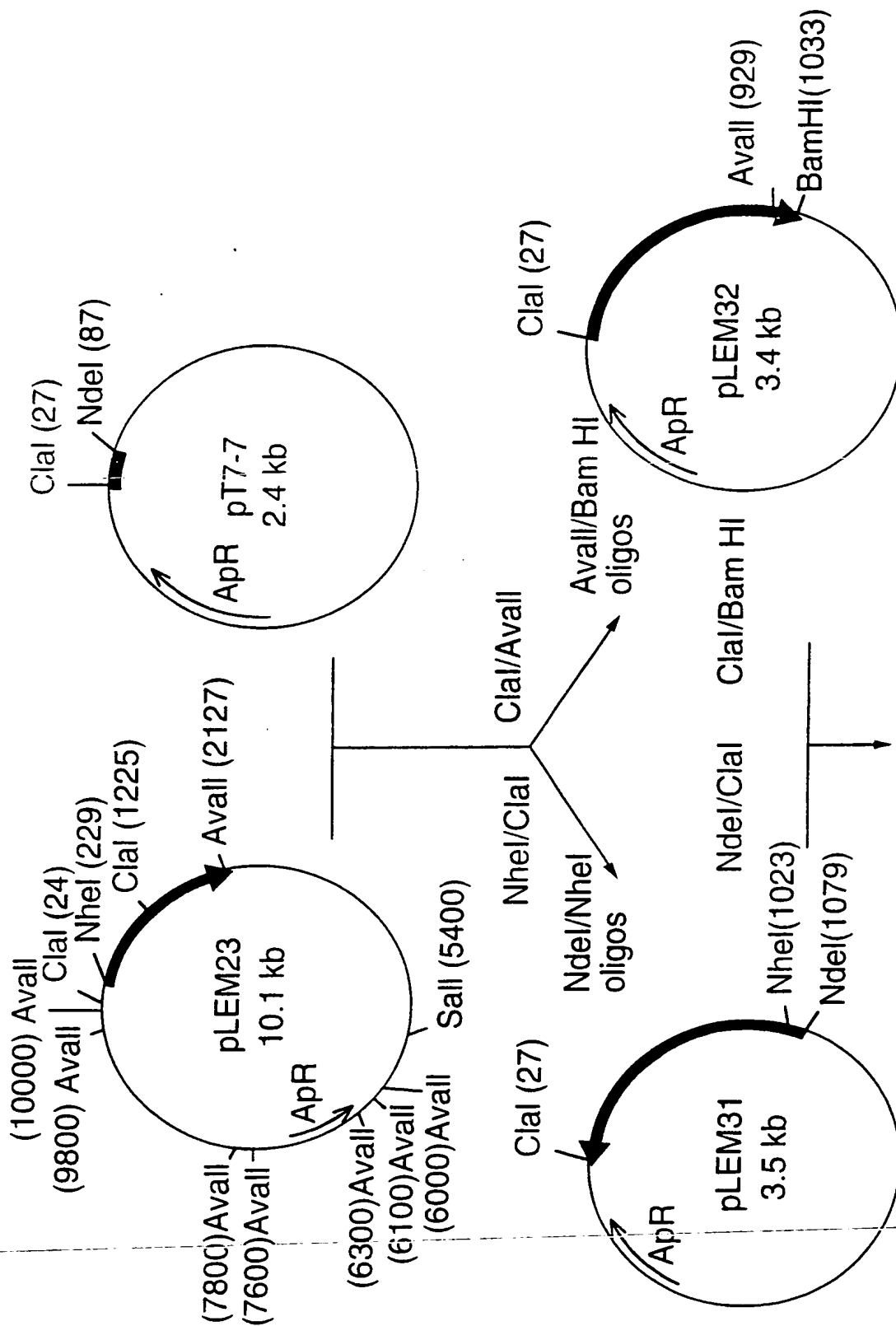
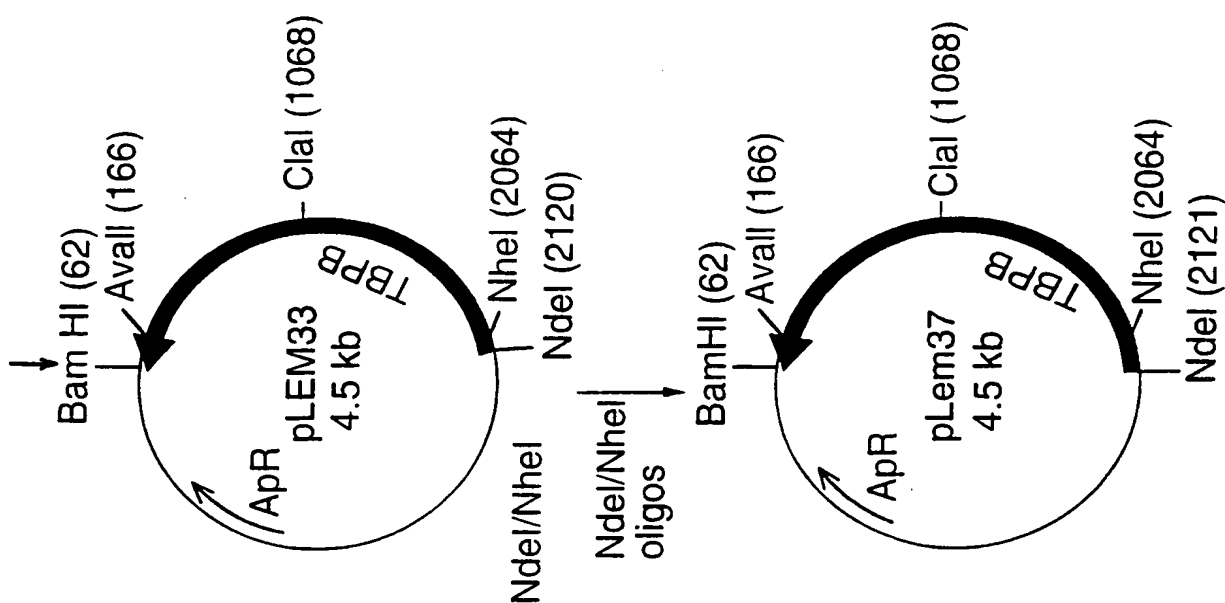


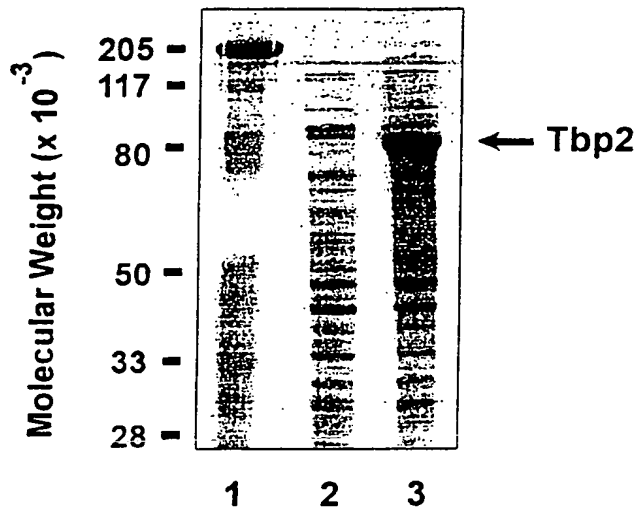
FIG.18A

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

FIG.18B



## Expression of rTbp2 in *E. coli*



1. Prestained molecular weight markers
2. pLEM37B-2 lysate, non-induced
3. pLEM37B-2 lysate, induced

Fig.19

O.G. FIG.	
APPROVED	CLASS
BY	SUBCLASS
DRAFTSMAN	

660750-8234760

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

660160-8294160

WO 97/32980

78/90

PCT/CA97/00163

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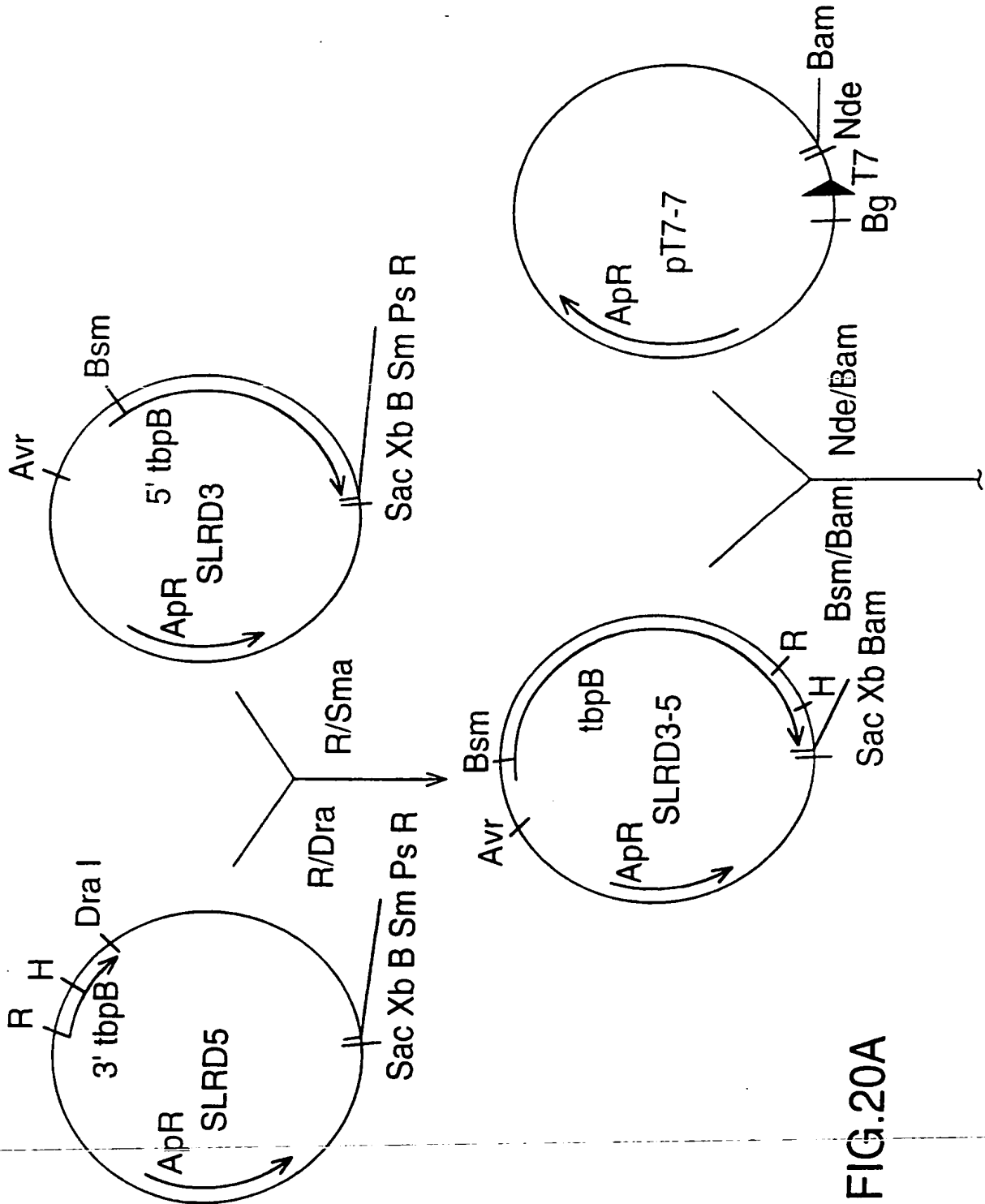


FIG.20A

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

600750" 82547160

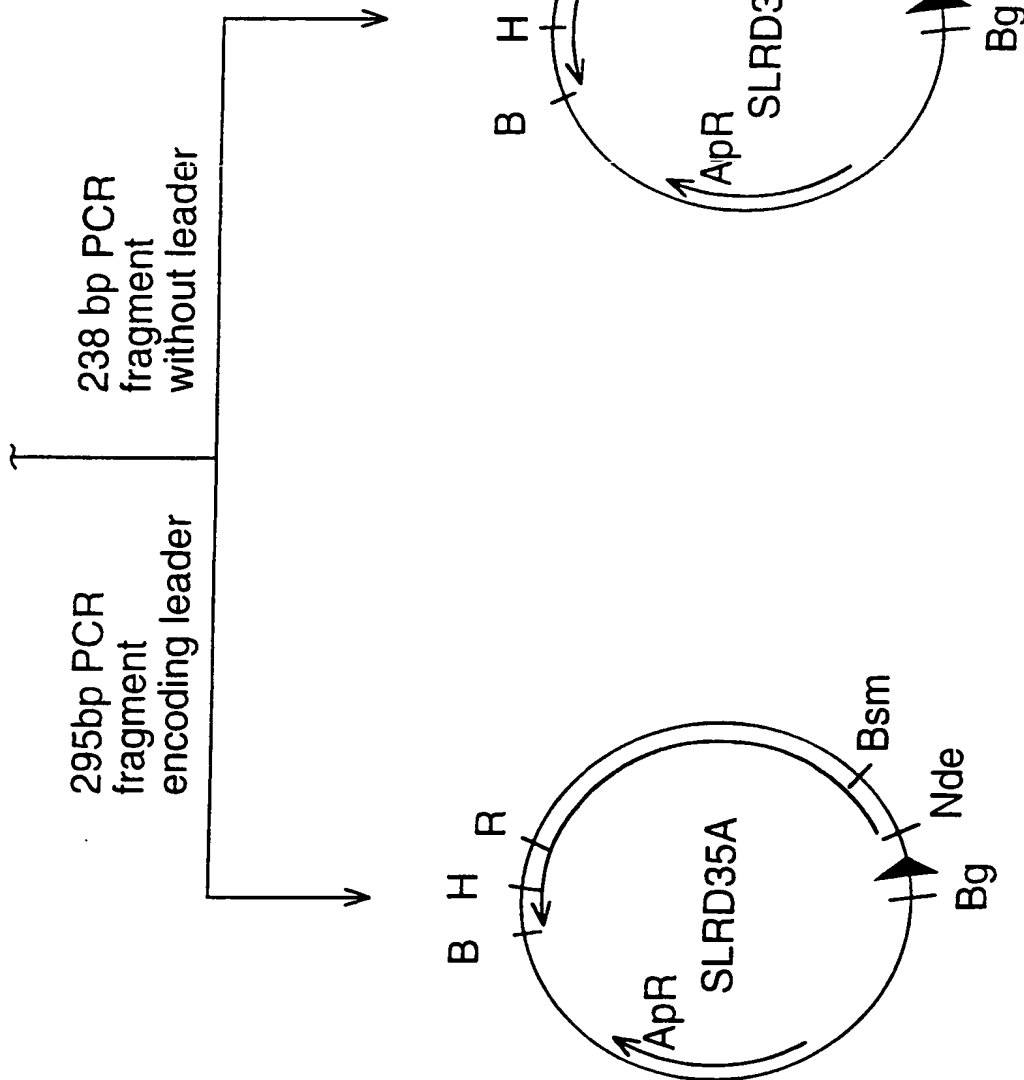
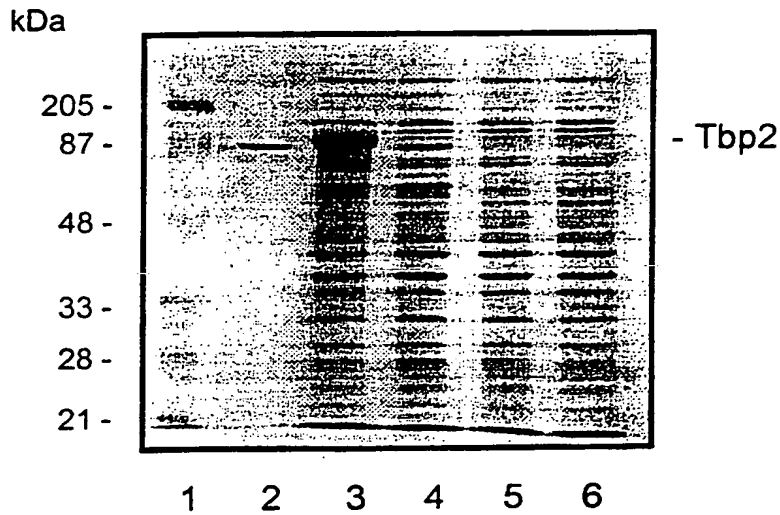


FIG.20B

Fig 21. Expression of Q8 rTbp2 protein in *E. coli*

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY		
DRAFTSMAN		



1. Prestained molecular weight markers
2. 4223 rTbp2 protein
3. SLRD35A lysate, 3 hr post-induction
4. SLRD35B lysate, 3 hr post-induction
5. SLRD35A lysate, non-induced
6. SLRD35B lysate, non-induced

660450-8292760



APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

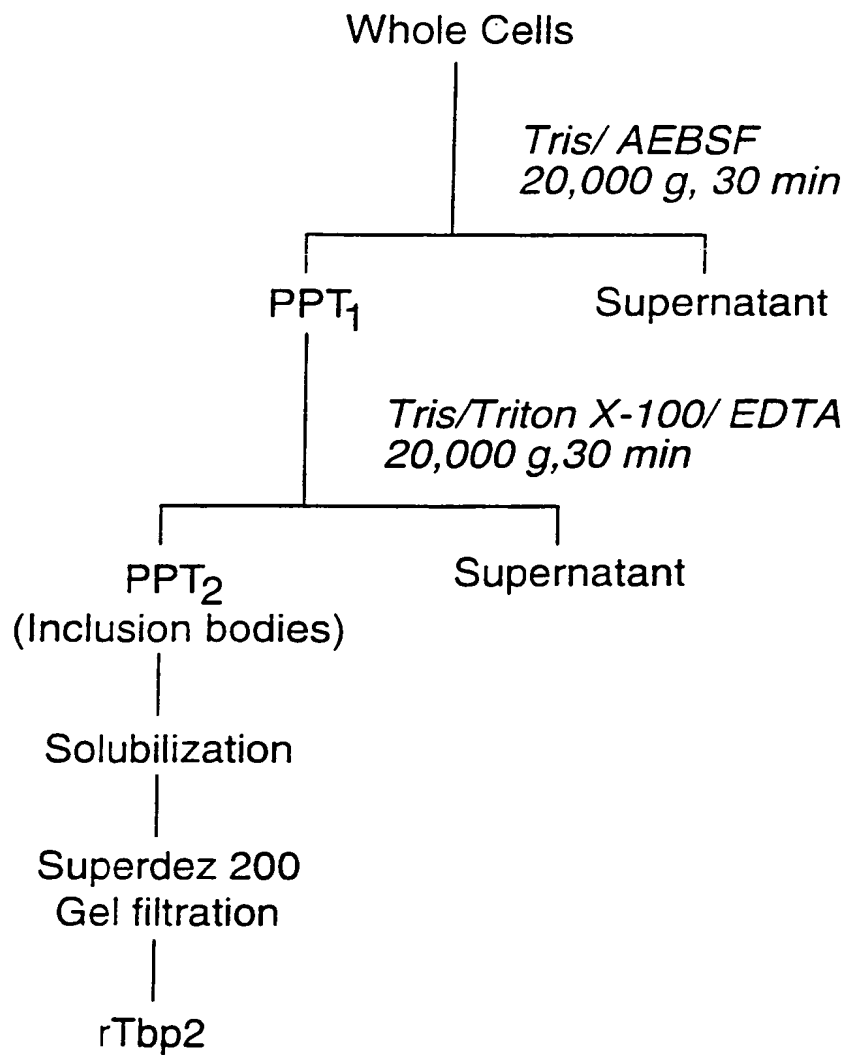
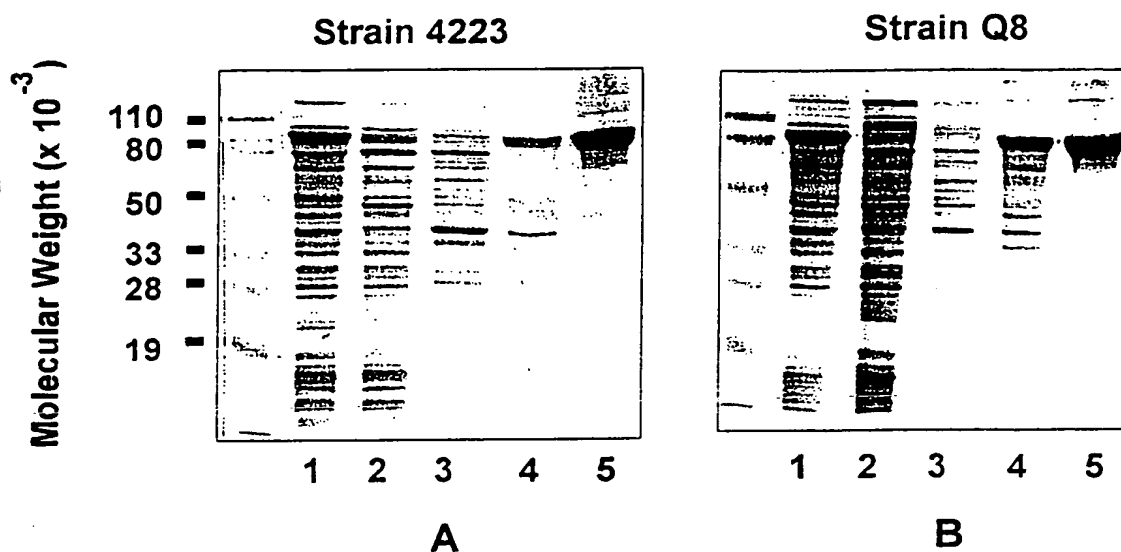
Purification of Tbp2 from *E.Coli*

FIG.22

O.G. FIG.	
CLASS	SUBCLASS
APPROVED BY	CRAFTSMAN

## Purification of rTbp2 from *E. coli*

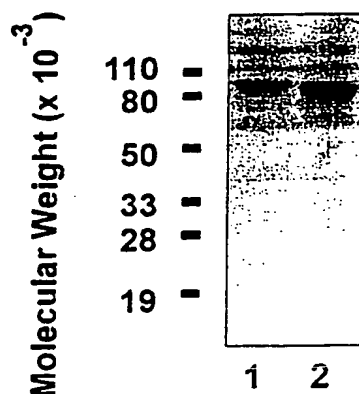


1. *E. coli* Whole cells
2. Soluble proteins after 50 mM Tris extraction
3. Soluble proteins after Tris/ Triton X-100/ EDTA extraction
4. Left-over pellet (rTbp2 inclusion bodies)
5. Purified rTbp2

**Fig.23**

APPROVED BY CRAFTSMAN	O.G. FIG.
	CLASS SUBCLASS

# Binding of Tbp2 to Human Transferrin



1. rTbp2 (strain 4223)
2. rTbp2 (strain Q8)

Fig.24

O.G. FIG.	
APPROVED	BY
CLASS SUBCLASS	
DRAFTSMAN	

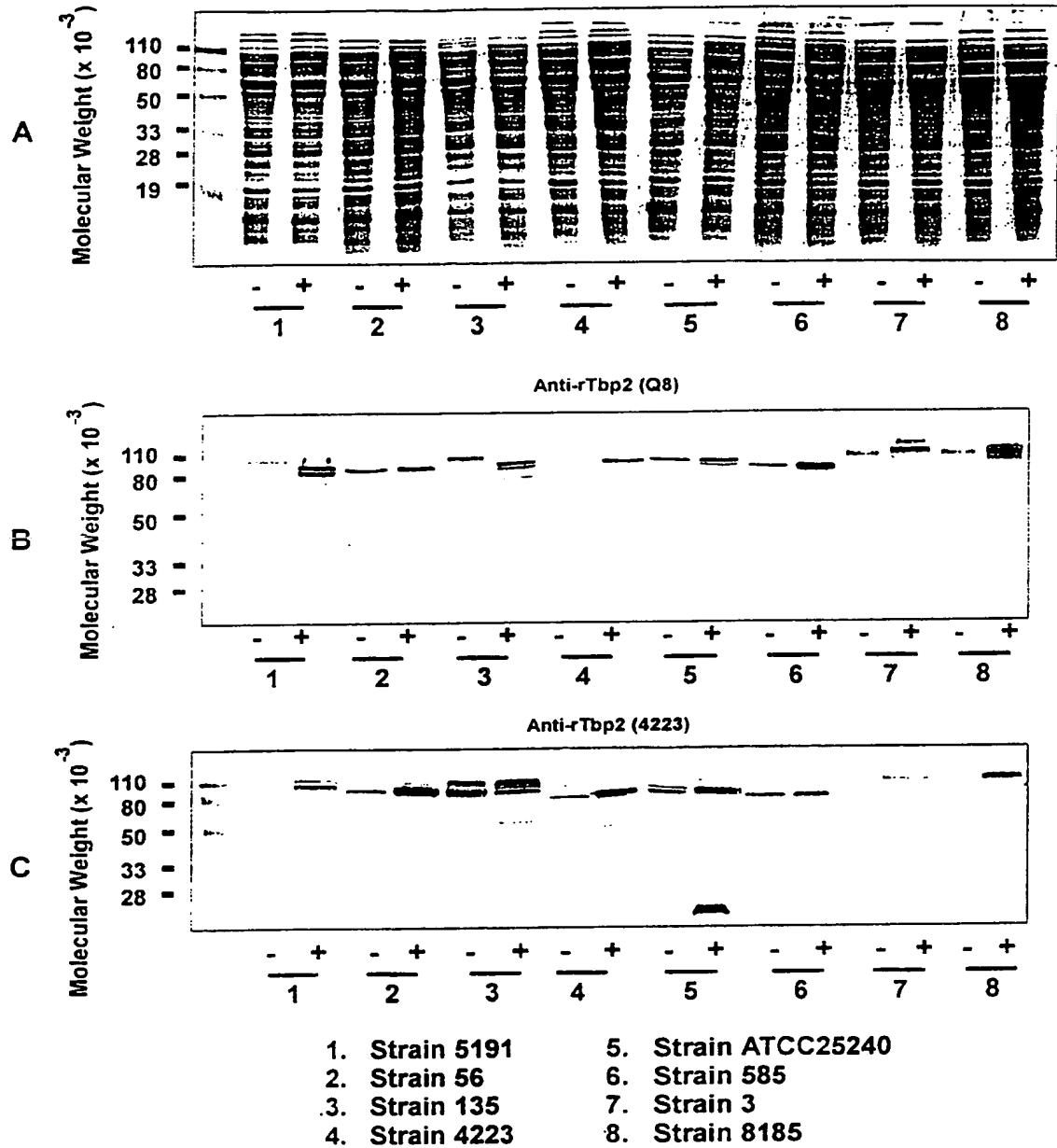
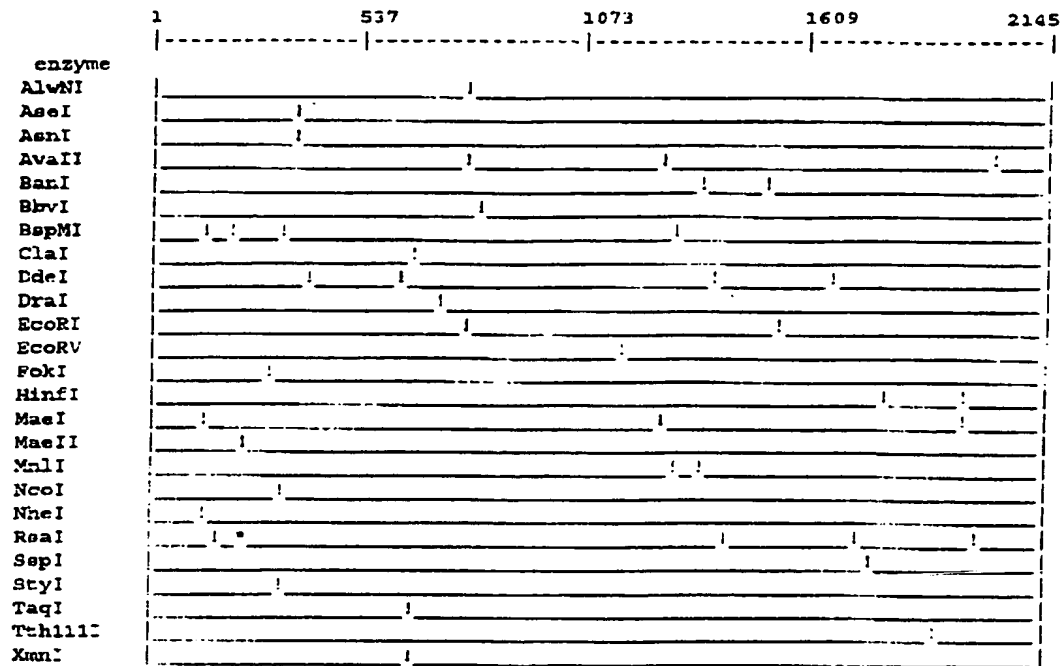


Fig.25

Figure 26 Restriction map of *M. catarrhalis* strain R1 *tbpB*

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

660130-32341150

Figure 27 Nucleotide and deduced amino acid sequence of *M. catarrhalis* R1 *tbpB*

AAATTTGCCGTATTTTGTCTATCATAAATGCATTTATCATCAATGCCCAAACAAATACGCCAAATGCACAT

TGTCAGCATGCCAAATAGGCATTAACAGACTTTTTTAGATAATACCATCAACCCATCAGAGGATTATTTT

27 54  
 ATG AAA CAC ATT CCT TTA ACC ACA CTG TGT GTG GCA ATC TCT GCC GTC TTA TTA  
 MET Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val Leu Leu

81 108  
 ACC GCT TGT GGT GGC AGT GGT GGT TCA AAT CCA CCT GCT CCT ACG CCC ATT CCA  
 Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro Thr Pro Ile Pro

135 162  
 AAT GCT AGC GGT TCA GGT AAT ACT GGC AAC ACT GGT AAT GCT GGC GGT ACT GAT  
 Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly Asn Ala Gly Gly Thr Asp

189 216  
 AAT ACA GCC AAT GCA GGT AAT ACA GGC GGT ACA AGC TCT GGT ACA GGC AGT GCC  
 Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly Thr Ser Ser Gly Thr Gly Ser Ala

243 270  
 AGC ACG TCA GAA CCA AAA TAT CAA GAT GTG CCA ACA ACG CCC AAT AAC AAA GAA  
 Ser Thr Ser Glu Pro Lys Tyr Gln Asp Val Pro Thr Thr Pro Asn Asn Lys Glu

297 324  
 CAA GTT TCA TCC ATT CAA GAA CCT GCC ATG GGT TAT GGC ATG GCT TTG AGT AAA  
 Gln Val Ser Ser Ile Gln Glu Pro Ala MET Gly Tyr Gly MET Ala Leu Ser Lys

351 378  
 ATT AAT CTA TAC GAC CAA CAA GAC ACG CCA TTA GAT GCA AAA AAT ATC ATT ACC  
 Ile Asn Leu Tyr Asp Gln Gln Asp Thr Pro Leu Asp Ala Lys Asn Ile Ile Thr

405 432  
 TTA GAC GGT AAA AAA CAA GTT GCT GAC AAT CAA AAA TCA CCA TTG CCA TTT TCG  
 Leu Asp Gly Lys Lys Gln Val Ala Asp Asn Gln Lys Ser Pro Leu Pro Phe Ser

459 486  
 TTA GAT GTA GAA AAT AAA TTG CTT GAT GGC TAT ATA GCA AAA ATG AAT GAA GCG  
 Leu Asp Val Glu Asn Lys Leu Leu Asp Gly Tyr Ile Ala Lys MET Asn Glu Ala

513 540  
 GAT AAA AAT GCC ATT GGT GAA AGA ATT AAG AGA GAA AAT GAA CAA AAT AAA AAA  
 Asp Lys Asn Ala Ile Gly Glu Arg Ile Lys Arg Glu Asn Glu Gln Asn Lys Lys

567 594  
 ATA TCC GAT GAA GAA CTT GCC AAA AAA ATC AAA GAA AAT GTG CGT AAA AGC CCT  
 Ile Ser Asp Glu Glu Leu Ala Lys Lys Ile Lys Glu Asn Val Arg Lys Ser Pro

621 648  
 GAG TTT CAG CAA GTA TTA TCA TCG ATA AAA GCG AAA ACT TTC CAT TCA AAT GAC  
 Glu Phe Gln Gln Val Leu Ser Ser Ile Lys Ala Lys Thr Phe His Ser Asn Asp

O.G. FIG.	CLASS	SUBCLASS
	APPROVED BY	DRAFTSMAN

600T30-22924160

87/90

FIG 27 (cont.)

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
	DRAFTSMAN	

[illegible]

AAA ACA ACC AAA GCA ACC ACA CGA GAT TTA AAA TAT GTT GAT TAT GGT TAC TAC	675	702
Lys Thr Thr Lys Ala Thr Thr Arg Asp Leu Lys Tyr Val Asp Tyr Gly Tyr Tyr		
TTG GTG AAT GAT GCC AAT TAT CTA ACC GTC AAA ACA GAC AAC CCA AAA CTT TGG	729	756
Leu Val Asn Asp Ala Asn Tyr Leu Thr Val Lys Thr Asp Asn Pro Lys Leu Trp		
AAT TCA GGT CCT GTG GGC GGT GTG TTT TAT AAT GGC TCA ACG ACC GCC AAA GAG	783	810
Asn Ser Gly Pro Val Gly Gly Val Phe Tyr Asn Gly Ser Thr Thr Ala Lys Glu		
CTG CCC ACA CAA GAT GCG GTC AAA TAT AAA GGA CAT TGG GAC TTT ATG ACC GAT	837	864
Leu Pro Thr Gln Asp Ala Val Lys Tyr Lys Gly His Trp Asp Phe MET Thr Asp		
GTT GCC AAA AAA AGA AAC CGA TTT AGC GAA GTA AAA GAA ACC TAT CAA GCA GGC	891	918
Val Ala Lys Lys Arg Asn Arg Phe Ser Glu Val Lys Glu Thr Tyr Gln Ala Gly		
TGG TGG TAT GGG GCA TCT TCA AAA GAT GAA TAC AAC CGC TTA TTA ACC AAA GCA	945	972
Trp Trp Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu Thr Lys Ala		
GAT GCC GCA CCT GAT AAT TAT AGC GGT GAA TAT GGT CAT AGC AGT GAA TTT ACT	999	1026
Asp Ala Ala Pro Asp Asn Tyr Ser Gly Glu Tyr Gly His Ser Ser Glu Phe Thr		
GTT AAT TTT AAG GAA AAA AAA TTA ACA GGT GAG CTG TTT AGT AAC CTA CAA GAC	1053	1080
Val Asn Phe Lys Glu Lys Lys Leu Thr Gly Glu Leu Phe Ser Asn Leu Gln Asp		
AGC CAT AAA CAA AAA GTA ACC AAA ACA AAA CGC TAT GAT ATT AAG GCT GAT ATC	1107	1134
Ser His Lys Gln Lys Val Thr Lys Thr Lys Arg Tyr Asp Ile Lys Ala Asp Ile		
CAC GGC AAC CGC TTC CGT GGC AGT GCC ACC GCA AGC GAT AAG GCA GAA GAC AGC	1161	1188
His Gly Asn Arg Phe Arg Gly Ser Ala Thr Ala Ser Asp Lys Ala Glu Asp Ser		
AAA AGC AAA CAC CCC TTT ACC AGC GAT GCC AAA GAT AAG CTA GAA GGT GGT TTT	1215	1242
Lys Ser Lys His Pro Phe Thr Ser Asp Ala Lys Asp Lys Leu Glu Gly Gly Phe		
TAT GGA CCA AAA GGC GAG GAG CTG GCA GGT AAA TTC TTA ACC GAT GAT AAC AAA	1269	1296
Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn Lys		
CTC TTT GGT GTC TTT GGT GCC AAA CAA GAG GGT AAT GTA GAA AAA ACC GAA GCC	1323	1350
Leu Phe Gly Val Phe Gly Ala Lys Gln Glu Gly Asn Val Glu Lys Thr Glu Ala		

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

SECRET

1377 1404  
ATC TTA GAT GCT TAT GCA CTT GGG ACA TTT AAT AAA CCT GGT ACG ACC AAT CCC  
Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Lys Pro Gly Thr Thr Asn Pro

1431 1458  
GCC TTT ACC GCT AAC AGC AAA AAA GAA CTG GAT AAC TTT GGC AAT GCC AAA AAG  
Ala Phe Thr Ala Asn Ser Lys Lys Glu Leu Asp Asn Phe Gly Asn Ala Lys Lys

1485 1512  
TTG GTC TTG GGT TCT ACC GTC ATT GAT TTG GTG CCT ACT GAT GCC ACC AAA GAT  
Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Asp Ala Thr Lys Asp

1539 1566  
GTC AAT GAA TTC AAA GAA AAG CCA AAG TCT GCC ACA AAC AAA GCG GGC GAA ACT  
Val Asn Glu Phe Lys Glu Lys Pro Lys Ser Ala Thr Asn Lys Ala Gly Glu Thr

1593 1620  
TTG ATG GTG AAT GAT GAA GTT AGC GTC AAA ACC TAT GGC AAA AAC TTT GAA TAC  
Leu MET Val Asn Asp Glu Val Ser Val Lys Thr Tyr Gly Lys Asn Phe Glu Tyr

1647 1674  
CTA AAA TTT GGT GAG CTT AGT GTC GGT GGT AGC CAT AGC GTC TTT TTA CAA GGC  
Leu Lys Phe Gly Glu Leu Ser Val Gly Gly Ser His Ser Val Phe Leu Gln Gly

1701 1728  
GAA CGC ACC GGT ACC ACA GGC GAG AAA GCC GTA CCA ACC ACA GGC AAA GCC AAA  
Glu Arg Thr Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Thr Gly Lys Ala Lys

1755 1782  
TAT TTG GGG AAC TGG GTA GGA TAT ATC ACA GGA GCG GAC TCA TCA AAA GGC TCT  
Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Ala Asp Ser Ser Lys Gly Ser

1809 1836  
ACC GAT GGC AAA GGC TTT ACC GAT GCC AAA GAT ATT GCT GAT TTT GAC ATT GAC  
Thr Asp Gly Lys Gly Phe Thr Asp Ala Lys Asp Ile Ala Asp Phe Asp Ile Asp

1863 1890  
TTT GAG AAA AAA TCA GTT AAT GGC AAA CTG ACC ACC AAA GAC CGC CAA GAC CCT  
Phe Glu Lys Lys Ser Val Asn Gly Lys Leu Thr Thr Lys Asp Arg Gln Asp Pro

1917 1944  
GTC TTT AAC ATC ACA GGT GAA ATC GCA GGC AAT GGC TGG ACA GGT AAA GCC AGC  
Val Phe Asn Ile Thr Gly Glu Ile Ala Gly Asn Gly Trp Thr Gly Lys Ala Ser

1971 1998  
ACC GCC GAA GCG AAC GCA GGG GGC TAT AAG ATA GAT TCT AGC AGT ACA GGC AAA  
Thr Ala Glu Ala Asn Ala Gly Gly Tyr Lys Ile Asp Ser Ser Ser Thr Gly Lys

2025 2052  
TCC ATC GTC ATC AAA GAT GCC GTG GTT ACA GGT GGC TTT TAT GGT CCA AAT GCA  
Ser Ile Val Ile Lys Asp Ala Val Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala



89/90

Fu 27 (cont)

2079

2106

ACC GAG ATG GGT GGG TCA TTT ACA CAC AAC AGC GGT AAT GAT GGT AAA GTC TCT  
 Thr Glu MET Gly Gly Ser Phe Thr His Asn Ser Gly Asn Asp Gly Lys Val Ser

2133

GTG GTC TTT GGC ACA AAA AAA CAA GAA GTT AAG AAG TGA  
 Val Val Phe Gly Thr Lys Lys Gln Glu Val Lys Lys \*

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

060150-82341160

### Alignment of *M. catarrhalis* Tbp2

[illegible][illegible]